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OM protein - protein search, using sw model

Run on: April 28, 2005, 13:57:35 ; Search time 122.5 Seconds
(without alignments)
56.830 Million cell updates/sec

Title: US-10-009-317A-32

Perfect score: 116

Sequence: 1 GFCRCICTRGFCRCICTR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : A_Geneseq_16Dec04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	116	100.0	18	4	AAB35046	Aab35046 Theta def
2	116	100.0	18	5	ABP53295	Abp53295 Anti-vira
3	116	100.0	18	8	ADO35230	Ado35230 Rhesus th
4	111	95.7	18	8	ADO35240	Ado35240 Rhesus th
5	103	88.8	18	5	ABP53299	Abp53299 Anti-vira
6	101	87.1	18	4	AAB35030	Aab35030 Theta def
7	101	87.1	18	5	ABP53297	Abp53297 Anti-vira
8	101	87.1	18	6	AAE33866	Aae33866 Macaca mu
9	101	87.1	18	7	ADN95202	Adn95202 Cyclic de
10	101	87.1	18	8	ADP33557	Adp33557 Antimicro
11	101	87.1	18	8	ADG70012	Adg70012 Rhesus th
12	101	87.1	18	8	ADO35229	Ado35229 Rhesus th
13	101	87.1	18	8	ADO35238	Ado35238 Rhesus th
14	101	87.1	18	8	ADO35239	Ado35239 Rhesus th
15	101	87.1	18	8	ADO35250	Ado35250 Rhesus th
16	101	87.1	18	8	ADO35263	Ado35263 Monkey RT
17	100	86.2	18	8	ADO35255	Ado35255 Rhesus th
18	93	80.2	18	6	AAE33805	Aae33805 I2Y retro
19	93	80.2	18	6	AAE33806	Aae33806 I11Y retr
20	93	80.2	18	8	ADN08180	Adn08180 Human ret
21	93	80.2	18	8	ADN08181	Adn08181 Human ret
22	91	78.4	18	4	AAB35037	Aab35037 Rhesus ma
23	90	77.6	18	5	ABP53294	Abp53294 Synthetic
24	90	77.6	18	6	AAE33801	Aae33801 Human ret
25	90	77.6	18	6	AAE33863	Aae33863 Enantio-r

26	90	77.6	18	8	ADN08176	Adn08176 Human ret
27	89	76.7	18	8	ADO35249	Ado35249 Rhesus th
28	88	75.9	18	5	ABP53298	Abp53298 Anti-vira
29	87	75.0	18	5	AAU91017	Aau91017 Transplan
30	87	75.0	18	6	AAE33864	Aae33864 Enantio-R
31	87	75.0	18	6	AAE33802	Aae33802 R9K retro
32	87	75.0	18	8	ADN08177	Adn08177 Human ret
33	86	74.1	18	4	AAB35047	Aab35047 Theta def
34	86	74.1	18	5	ABP53296	Abp53296 Anti-vira
35	86	74.1	18	8	ADO35231	Ado35231 Rhesus th
36	86	74.1	18	8	ADO35242	Ado35242 Rhesus th
37	86	74.1	18	8	ADO35241	Ado35241 Rhesus th
38	85	73.3	18	6	AAE33804	Aae33804 I15Y retr
39	85	73.3	18	6	AAE33803	Aae33803 I6Y retro
40	85	73.3	18	8	ADO35256	Ado35256 Rhesus th
41	85	73.3	18	8	ADN08179	Adn08179 Human ret
42	85	73.3	18	8	ADN08178	Adn08178 Human ret
43	83	71.6	18	6	AAE33807	Aae33807 R4Y retro
44	83	71.6	18	8	ADO35246	Ado35246 Rhesus th
45	83	71.6	18	8	ADO35245	Ado35245 Rhesus th

ALIGNMENTS

RESULT 1
AAB35046
ID AAB35046 standard; peptide; 18 AA.

XX AAB35046;

AC AAB35046;

DT 27-MAR-2001 (first entry)

DE Theta defensin SEQ ID NO: 30.

XX Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan;

KW virus; helminth; disinfectant; food preservative; analogue.

XX Unidentified.

XX WO2000068265-A1.

XX 16-NOV-2000.

XX 10-MAY-2000; 2000WO-US012842.

XX 10-MAY-1999; 99US-00309487.

XX (REGC) UNIV CALIFORNIA.

XX Selsted ME, Tang Y, Yuan J, Ouellette AJ;

XX WPI; 2001-031853/04.

XX Novel theta defensin peptide with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses.

XX Claim 15; Fig 16; 110pp; English.

XX The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives

XX Sequence 18 AA;

Query Match 100.0%; Score 116; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFCRCICTRGFCRCICTR 18
| | | | | | | | | | | | | | | | | |
Db 1 GFCRCICTRGFCRCICTR 18

current apphct
- priority document

RESULT 2
ID ABP53295 standard; peptide; 18 AA.
XX
AC ABP53295;
XX
DT 13-NOV-2002 (first entry)
XX
DE Anti-viral theta defensin peptide RTD-2 SEQ ID NO:28.
XX
KW Anti-viral; viral infection; theta-defensin; lipid environment;
KW amphipathic alpha-helical structure; virucide; anti-HIV; immunisation;
KW viral growth inhibitor; viral proliferation inhibitor.
XX
OS Macaca mulatta.
OS Synthetic.
XX
FN WO200260468-A2.
XX
PD 08-AUG-2002.
XX
FF 29-JAN-2002; 2002WO-US002435.
XX
PR 30-JAN-2001; 2001US-0265270P.
PR 01-AUG-2001; 2001US-0309368P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
FI Maury W, Stapleton J, Stinski M, Rollier R, McCray PB, Tack B;
XX WPI; 2002-674815/72.
XX
PT New method of using a first anti-viral peptide comprising a Theta-
PT defensin peptide in an amphipathic Alpha-helical structure in a lipid
PT environment for reducing the infectivity of a virus.
XX
PS Disclosure; Page 10; 65pp; English.
XX
CC The present invention describes a method (M1) of using a first anti-viral
CC peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-
CC helical structure in a lipid environment for reducing the infectivity of
CC a virus. (I) can have virucide and anti-HIV activities, and can be used
CC to reduce virus growth, infectivity burden, shed, and development of anti
CC -viral resistance. (I) can be used for inhibiting the growth and
CC proliferation of a virus and so can be used for; (a) protecting or
CC treating subject from a viral infection, preventing recurrent viral
CC infection in a subject harbouring a latent virus, controlling virus
CC spread within a virally-infected subject (VS), reducing viral burden in a
CC VS, reducing virus shed from a VS, reducing percentage of VS in a
CC population regardless of viral infection status, or inducing latency in a
CC VS; (b) reducing the infectivity of a virus; and (c) rendering virus-
CC contaminated tissue or fluid sample safe for use, or reducing the number
CC of infectious virus particles in a population of viruses. (M1) is useful
CC for reducing the infectivity of a virus in sheep, cattle, horses, swine,
CC cats, fowl and humans e.g. an enveloped virus infecting humans such as
CC human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is
CC administered to a patient who is immunosuppressed or to a subject who is
CC not infected with the virus, where the first anti-viral peptide is
CC administered prior to or subsequent to the virus contacting the subject.
CC The anti-viral peptide is most preferably administered to a subject who
CC is chronically, latently or acutely infected with the virus. The present
CC sequence represents a rhesus monkey theta defensin anti-viral peptide,
CC which is given in the exemplification of the present invention
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 116; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFCRCICTRGFCRCICTR 18

Db 1 GFCRCICTRGFCRCICTR 18
RESULT 3
ADO35230
ID ADO35230 standard; peptide; 18 AA.
XX
AC ADO35230;
XX
DT 15-JUL-2004 (first entry)
XX
DE Rhesus theta defensin peptide, RTD-2.
XX
KW Monkey; Rhesus theta defensin; RTD-2; antimicrobial peptide; cyclic;
KW antimicrobial; antiinflammatory; antibacterial; virucide; fungicide;
KW food; contact lens solution; eye wash solution; inflammatory response;
KW microbicidal inhibition; microstatic growth inhibition; disinfectant;
KW food preservative; bacterial infection; viral infection;
KW fungal infection; haemolytic activity.
XX
OS Macaca mulatta.
XX
FH Key Location/Qualifiers
FT Modified-site 1. 18
FT /note= "The peptide is cyclised by a covalent link
FT between these two residues"
FT Disulfide-bond 3. 16
FT Disulfide-bond 5. 14
FT Disulfide-bond 7. 12
XX
FN US2004014669-A1.
XX
PD 22-JAN-2004.
XX
PF 30-APR-2003; 2003US-00427715.
XX
PR 30-APR-2002; 2002US-0377071P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
FI Selsted ME, Tran DQ;
XX
DR WPI; 2004-167945/16.
XX
PT Novel theta defensin analog useful for reducing or inhibiting growth or
PT survival of a microorganism in an environment such as food or food
PT product, contact lens solution, or eye wash solution, an inanimate
XX object.
XX
PS Example 1; SEQ ID NO 2; 46pp; English.
XX
CC The invention relates to a theta defensin analogue defined by formulae
CC detailed in the claims or appearing as ADO35239-ADO35257. The theta
CC defensin analogue is useful for reducing or inhibiting growth or survival
CC of a microorganism in an environment capable of sustaining the growth or
CC survival of the microorganism and is useful for reducing or inhibiting
CC growth or survival of a microorganism in an environment such as food or
CC food product, a solution (e.g., contact lens solution, or eye wash
CC solution), an inanimate object comprising surface, or a mammal. The
CC peptides are also useful for decreasing inflammatory response and for
CC microbicidal inhibition of survival of microorganism as well as
CC microstatic inhibition of growth. Thus the peptides are useful as
CC therapeutic agents, disinfectants, food preservatives, or medicaments.
CC The peptides are also useful for treating a patient suffering from
CC bacterial, viral, fungal or other infection. The theta defensins have
CC high antimicrobial activity and low haemolytic activity. The present
CC sequence represents the rhesus monkey wild-type theta defensin RTD-2.
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 116; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;

DR 1536

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCICICTR 18
Db 1 GFCRCICTRGFCICICTR 18

RESULT 4
ID ADO35240 standard; peptide; 18 AA.

XX ADO35240;

XX 15-JUL-2004 (first entry)

XX Rhesus theta defensin analogue peptide arTD-2-OH.

XX Monkey; Rhesus theta defensin; RPD; antimicrobial peptide; antimicrobial;
XX antiinflammatory; antibacterial; virucide; fungicide; food;
XX contact lens solution; eye wash solution; inflammatory response;
XX microbicidal inhibition; microbiostatic growth inhibition; disinfectant;
XX food preservative; bacterial infection; viral infection;
XX fungal infection; haemolytic activity.

XX Macaca mulatta.
XX Synthetic.

Key Location/Qualifiers
FT Disulfide-bond 3. .16
FT Disulfide-bond 5. .14
FT Disulfide-bond 7. .12
FT Modified-site 18
FT /note= "Hydroxylated"

XX US2004014669-A1.

XX 22-JAN-2004.

XX 30-APR-2003; 2003US-00427715.

XX 30-APR-2002; 2002US-0377071P.

XX (REGC) UNIV CALIFORNIA.

XX Selected ME, Tran DQ;

XX WPI; 2004-167945/16.

XX Novel theta defensin analog useful for reducing or inhibiting growth or
XX survival of a microorganism in an environment such as food or food
XX product, contact lens solution, or eye wash solution, an inanimate
XX object.

XX Claim 1; SEQ ID NO 14; 46pp; English.

XX The invention relates to a theta defensin analogue defined by formulae
XX detailed in the claims or appearing as ADO35239-ADO35257. The theta
XX defensin analogue is useful for reducing or inhibiting growth or survival
XX of a microorganism in an environment capable of sustaining the growth or
XX survival of the microorganism and is useful for reducing or inhibiting
XX growth or survival of a microorganism in an environment such as food or
XX food product, a solution (e.g., contact lens solution, or eye wash
XX solution), an inanimate object comprising surface, or a mammal. The
XX peptides are also useful for decreasing inflammatory response and for
XX microbicidal inhibition of survival of microorganism as well as
XX microbiostatic inhibition of growth. Thus the peptides are useful as
XX therapeutic agents, disinfectants, food preservatives, or medicaments.
XX The peptides are also useful for treating a patient suffering from
XX bacterial, viral, fungal or other infection. The theta defensins have
XX high antimicrobial activity and low haemolytic activity. The present
XX sequence represents a Rhesus theta defensin analogue peptide.

XX Sequence 18 AA;

Query Match 95.7%; Score 111; DB 8; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.8e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCICICTR 18
Db 1 GFCRCICTRGFCICICTR 18

RESULT 5

ID ABP53299 standard; peptide; 18 AA.

XX ABP53299;

XX 13-NOV-2002 (first entry)

XX Anti-viral chimeric theta defensin peptide H/RTD-2 SEQ ID NO:32.

XX Anti-viral; viral infection; theta-defensin; lipid environment;
XX amphipathic alpha-helical structure; virucide; anti-HIV; immunisation;
XX viral growth inhibitor; viral proliferation inhibitor.

XX Homo sapiens.
XX Macaca mulatta.
XX Synthetic.

XX WO200260468-A2.

XX 08-AUG-2002.

XX 29-JAN-2002; 2002WO-US002435.

XX 30-JAN-2001; 2001US-0265270P.

XX 01-AUG-2001; 2001US-030368P.

XX (IOWA) UNIV IOWA RES FOUND.

XX Maury W, Stapleton J, Stinski M, Rollier R, Mccray PB, Tack B;

XX WPI; 2002-674815/72.

XX New method of using a first anti-viral peptide comprising a Theta-
XX defensin peptide in an amphipathic Alpha-helical structure in a lipid
XX environment for reducing the infectivity of a virus.

XX Disclosure; Page 10; 65pp; English.

XX The present invention describes a method (M1) of using a first anti-viral
XX peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-
XX helical structure in a lipid environment for reducing the infectivity of
XX a virus. (I) can have virucide and anti-HIV activities, and can be used
XX to reduce virus growth, infectivity burden, shed, and development of anti
XX -viral resistance. (I) can be used for inhibiting the growth and
XX proliferation of a virus and so can be used for; (a) protecting or
XX treating subject from a viral infection, preventing recurrent viral
XX infection in a subject harbouring a latent virus, controlling virus
XX spread within a virally-infected subject (VS), reducing viral burden in a
XX VS, reducing virus shed from a VS, reducing percentage of VS in a
XX population regardless of viral infection status, or inducing latency in a
XX VS; (b) reducing the infectivity of a virus; and (c) reducing the number
XX of infectious virus particles in a population of viruses. (M1) is useful
XX for reducing the infectivity of a virus in sheep, cattle, horses, swine,
XX cats, fowl and humans e.g. an enveloped virus infecting humans such as
XX human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is
XX administered to a patient who is immunosuppressed or to a subject who is
XX not infected with the virus, where the first anti-viral peptide is
XX administered prior to or subsequent to the virus contacting the subject.
XX The anti-viral peptide is most preferably administered to a subject who
XX is chronically, latently or acutely infected with the virus. The present
XX sequence represents a chimeric human/rhesus monkey theta defensin anti-

CC viral peptide, which is given in the exemplification of the present
CC invention

XXXXXXXXXXXX

Sequence 18 AA;

```
Query Match      88.8%; Score 103; DB 5; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.0002;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 GFCRCICTRGFCRCICTR 18
| | | | | | | | | |
Db 1 GICRCICTRGFCRCICGR 18

RESULT 6
AAB35030
ID AAB35030 standard; peptide: 18 AA.

AAC 35030:

2000

DT 27-MAR-2001 (first entry)

XX
XX

DE Theta defensin SEQ ID NO: 1.
XX
KW Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan;
KW virus; helminth; disinfectant; food preservative; analogue.

Unidentified.

XX
33
SUPPLEMENTED.

AA	Key	Location/Qualifiers
FH	Cross-links	1. .18
FT		

FT /note=

FT	Disulfide-bond	3.16
FT	Disulfide-bond	3.16

FT Disulfide-bond 5. .14

FT Disulfide-bond

XX

PN WO200068265-A1.

XX

PD 16-NOV-2000.

[illegible]

PF 10-MAY-2000; 2000WO-

XX
PR 10-MAY-1999; 99US-00309487.
yy

XX
PA (REGC) ITNIV CALITEORNTA

FA (REGC) / UNIV CALIFORNIA.
XX
XX Selsted ME, Tang Y, Yuan J, Ouellette AJ;
PI
XX
XX WPI; 2001-031853/04.
DR
XX
XX Novel theta defensin peptide with antimicrobial activity against
PT bacteria, yeast, fungi, protozoa and viruses.
PT
XX
XX Claim 4; Page 4; 110pp; English.
PS
XX
XX The present invention provides theta defensin peptides and analogues
CC which have antimicrobial activity. They can be used in the treatment of
CC bacterial, viral, fungal, protozoan and helminthic infections, in
CC disinfectants and as food preservatives

AA	Sequence 18 AA;	87.1%
SQ	Query Match	

RESULT 7
ABP53297

RESULT 8
 AAE33866
 ID AAE33866 standard; peptide; 18 AA.
 AC AAE33866;
 DT 16-APR-2003 (first entry)
 XX Macaca mulatta RTD1 peptide.
 DE
 XX
 KW Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV;
 KW human immunodeficiency virus; bacterial vaginosis; ophthalmic infection;
 KW antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1A;
 KW RTD1.
 XX
 OS Macaca mulatta.
 XX
 PN WO200285401-A1.
 XX
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US012353.
 XX
 PR 18-APR-2001; 2001US-0284855P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Lehrer RI, Waring AJ, Cole AM, Hong TB;
 XX WPI; 2003-103387/09.
 XX
 PT New isolated retrocyclin peptide, useful for preventing retroviral
 PT infections in cells susceptible to bacterial or viral infections or
 PT treating patients having the infections, such as HIV, sexually
 PT transmitted diseases, vaginosis.
 XX
 PS Example 1; Fig 3C; 72pp; English.
 XX
 CC The invention relates to novel retrocyclin peptides. Peptides and methods
 CC of the invention are useful for preventing retroviral infections in cells
 CC susceptible to bacterial or viral infections, or treating patients having
 CC infections such as HIV (human immunodeficiency virus), sexually
 CC transmitted diseases, bacterial vaginosis or ophthalmic infections. The
 CC retrocyclin-mediated killing is useful for modelling and screening novel
 CC antibiotics. The invention is also useful in gene therapy. The present
 CC sequence is rhesus monkey theta defensin, RTD1 peptide. This sequence is
 CC used in the exemplification of the invention
 XX
 SQ Sequence 18 AA;
 Query Match 87.1%; Score 101; DB 6; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00032;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GFCRCICTRGFCRCICTR 18
 Db 1 GVCRCICTRGFCRCICLR 18
 RESULT 9
 ADD95202
 ID ADD95202 standard; peptide; 18 AA.
 AC ADD95202;
 DT 29-JAN-2004 (first entry)
 XX
 DE Cyclic defensin fragment.
 XX
 KW bacterial infection; human pathogen; holin; defensin;
 KW peptide nucleic acid; PNA; penicillin; tetracycline; ampicillin;
 KW kanamycin; antibiotic; antibacterial; antibiotic-resistance gene; cyclic.
 XX

OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1. .18
 FT /note= "Residue 1 and residue 18 bond to form a cyclic
 FT moiety"
 FT Disulfide-bond 3. .16
 FT Disulfide-bond 5. .14
 FT Disulfide-bond 7. .12
 XX
 PN WO2003059392-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 17-JAN-2003; 2003WO-DE000124.
 XX
 PR 18-JAN-2002; 2002DE-01001862.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Braun K, Braun I, Debus J, Pipkorn R, Waldeck W;
 XX WPI; 2003-689464/65.
 DR
 XX New conjugate of transport mediator and active agent, useful for treating
 PT prokaryotic infections, especially by neutralizing antibiotic resistance
 PT gene.
 PT
 PS Disclosure; Fig 10; 34pp; German.
 XX
 CC This invention describes a novel conjugate for treating prokaryotic
 CC infections which comprises a transport mediator for passage through the
 CC prokaryotic cell membrane and a compound, directed against a prokaryote
 CC and intended for introduction into it. The prokaryote is a bacterium,
 CC especially one pathogenic in humans. The transport mediator is preferably
 CC a human peptide or protein, especially a phage-nolin protein, its active
 CC fragment or variant or a defensin. The introduced compound is a peptide
 CC nucleic acid (PNA) that inhibits a gene, especially one implicated in
 CC resistance to penicillin, tetracycline, ampicillin or kanamycin. The
 CC conjugate has the structure transport mediator-spacer-PNA where the
 CC spacer is poly(glycine and/or lysine), preferably containing 2-6 amino
 CC acids and the spacer is linked to the transport mediator through a
 CC cleavable disulfide bridge. The conjugates are administered together with
 CC an antibiotic, by parenteral, transdermal or subcutaneous routes. The
 CC products of the invention have antibacterial activity and are used,
 CC especially in combination with antibiotics, for treating prokaryotic,
 CC specifically bacterial, infections, especially where the pathogen is
 CC resistant to at least one antibiotic and then the PNA is directed against
 CC the antibiotic-resistance gene. Where the PNA is directed against an
 CC antibiotic resistance gene the conjugate will render the bacteria
 CC sensitive to co-administered antibiotics i.e. 'old' antibiotics can be
 CC used successfully in cases where normally they would be ineffective. This
 CC sequence represents a cyclic defensin fragment described in the
 CC disclosure of the invention.
 XX
 SQ Sequence 18 AA;
 Query Match 87.1%; Score 101; DB 7; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00032;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GFCRCICTRGFCRCICTR 18
 Db 1 GFCRCICRGVCRICICTR 18
 RESULT 10
 ADD35357
 ID ADD35357 standard; peptide; 18 AA.
 XX
 AC ADD35357;
 XX
 DT 15-JAN-2004 (first entry)

XX DE Antimicrobial peptide theta-defensin.
 XX DE antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological;
 KW intraocular pressure; glaucoma; ocular hypertension; hyperaemia;
 KW irritation; inflammation; conjunctiva; ocular cell dysplasia;
 KW iridial melanocyte hyperplasia; hyperpigmentation.
 XX OS Unidentified.
 XX OS WO2003079997-A2.
 XX FN 02-OCT-2003.
 XX PD 21-MAR-2003; 2003WO-US008935.
 XX PF 21-MAR-2002; 2002US-0367071P.
 XX PR (CAYM-) CAYMAN CHEM CO.
 XX PA Maxey KM, Johnson J;
 XX PI WPI; 2004-011506/01.
 XX DR Ophthalmic solution useful for the treatment of increased intraocular
 XX PT pressure comprises a prostaglandin of the F-series and an antimicrobial
 XX PT peptide.
 XX PS Disclosure; Page 11; 11pp; English.
 XX XX The invention relates to a novel ophthalmic solution comprising a
 XX CC prostaglandin of the F-series and an antimicrobial peptide. A solution of
 XX CC the invention has hypotensive and ophthalmological activity. The solution
 XX CC is useful for the treatment of increased intraocular pressure, such as
 XX CC caused by glaucoma and for the reduction of ocular hypertension. The
 XX CC prostaglandin and the antimicrobial peptide work synergistically, to
 XX CC provide beneficial reduction in the incidence of irritant and toxic side
 XX CC effects such as hyperaemia, irritation and inflammation of conjunctiva,
 XX CC ocular cell dysplasia, iridial melanocyte hyperplasia, and
 XX CC hyperpigmentation, associated with the prior art prostaglandin
 XX CC compositions. The present sequence represents an antimicrobial peptide of
 XX CC the invention.
 XX SQ Sequence 18 AA;
 XX
 XX Query Match 87.1%; Score 101; DB 8; Length 18;
 XX Best Local Similarity 83.3%; Pred. No. 0.00032;
 XX Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX QY 1 GFCRCICTRGFCRCICTR 18
 XX |||||:|||||
 XX DB 1 GFCRCICRRGVRCICTR 18
 XX
 XX RESULT 11
 XX ADG70012
 XX ID ADG70012 standard; peptide; 18 AA.
 XX AC ADG70012;
 XX DT 11-MAR-2004 (first entry)
 XX DE Rhesus theta-defensin-1 (RTD-1) peptide.
 XX KW rhesus theta defensin-1; RTD-1; bacteraemia; lipopolysaccharide; LPS;
 KW lipoteichoic acid; LTA; septic shock; antibacterial; fungicide; virucide;
 KW immunomodulator; anticoagulant activity;
 KW microbial cell-wall biosynthesis; immunomodulation; anticoagulant.
 XX OS Macaca mulatta.
 XX XX WO2003105883-A1.
 XX XX

PD 24-DEC-2003.
 XX 30-MAY-2003; 2003WO-EP005694.
 XX 13-JUN-2002; 2002DE-01026216.
 XX (FARB) BAYER HEALTHCARE AG.
 XX Ladel C, Newton B, Labischinski H, Brunner N, Gerdes C;
 XX WPI; 2004-071500/07.
 XX Use of rhesus theta defensin-1 for treating or preventing bacteremia and
 XX septic shock, also for binding bacterial products and as immunomodulator
 XX and anticoagulant.
 XX Example 1; SEQ ID NO 1; 28pp; German.
 XX This invention describes the novel use of rhesus theta defensin-1 (RTD-1)
 XX for preparing a composition for treatment and/or prevention of
 XX bacteraemia for binding bacterial products such as lipopolysaccharide
 XX (LPS) and/or lipoteichoic acid (LTA), or for treatment and/or prevention
 XX of septic shock. RTD-1, isolated from immune cells of rhesus monkeys, has
 XX antibacterial, fungicide, virucide, immunomodulator and anticoagulant
 XX activity. RTD-1 inhibits microbial cell-wall biosynthesis and also binds
 XX to LPS and LTA. RTD-1 is useful for treatment and prevention of severe
 XX infections caused by Gram-positive or -negative bacteria and yeasts, or
 XX by viruses. RTD-1 combines four advantageous properties: a direct
 XX antimicrobial action, neutralisation of bacterial products (by binding),
 XX immunomodulation (reducing release of proinflammatory cytokines but
 XX increasing release of regulatory factors) and anticoagulant action, so
 XX provides a better and simpler treatment.
 XX SQ Sequence 18 AA;
 XX
 XX Query Match 87.1%; Score 101; DB 8; Length 18;
 XX Best Local Similarity 83.3%; Pred. No. 0.00032;
 XX Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX QY 1 GFCRCICTRGFCRCICTR 18
 XX |||||:|||||
 XX DB 1 GFCRCICRRGVRCICTR 18
 XX
 XX RESULT 12
 XX ADO35229
 XX ID ADO35229 standard; peptide; 18 AA.
 XX AC ADO35229;
 XX DT 15-JUL-2004 (first entry)
 XX DE Rhesus theta defensin peptide, RTD-1.
 XX KW Monkey; Rhesus theta defensin; RTD-1; antimicrobial peptide; cyclic;
 KW antimicrobial; antiinflammatory; antibacterial; virucide; fungicide;
 KW food; contact lens solution; eye wash solution; inflammatory response;
 KW microbicidal inhibition; microbistatic growth inhibition; disinfectant;
 KW food preservative; bacterial infection; viral infection;
 KW fungal infection; haemolytic activity.
 XX OS Macaca mulatta.
 XX XX
 XX Key Location/Qualifiers
 XX Modified-site 1..18
 XX /note= "The peptide is cyclised by a covalent link
 XX between these two residues"
 XX Disulfide-bond 3..16
 XX Disulfide-bond 5..14
 XX Disulfide-bond 7..12
 XX US2004014669-A1.
 XX XX

PD 22-JAN-2004.
 XX 30-APR-2003; 2003US-00427715.
 XX 30-APR-2002; 2002US-0377071P.
 XX (REGC) UNIV CALIFORNIA.
 XX Selsted ME, Tran DQ;
 FI WPI; 2004-167945/16.
 DR Novel theta defensin analog useful for reducing or inhibiting growth or
 XX survival of a microorganism in an environment such as food or food
 XX product, contact lens solution, or eye wash solution, an inanimate
 XX object.
 XX Example 1; SEQ ID NO 1; 46pp; English.
 XX The invention relates to a theta defensin analogue defined by formulae
 CC detailed in the claims or appearing as ADO35239-ADO35257. The theta
 CC defensin analogue is useful for reducing or inhibiting growth or survival
 CC of a microorganism in an environment capable of sustaining the growth or
 CC survival of the microorganism and is useful for reducing or inhibiting
 CC growth or survival of a microorganism in an environment such as food or
 CC food product, a solution (e.g., contact lens solution, or eye wash
 CC solution), an inanimate object comprising surface, or a mammal. The
 CC peptides are also useful for decreasing inflammatory response and for
 CC microbicidal inhibition of survival of microorganism as well as
 CC therapeutic agents, disinfectants, food preservatives, or medicaments.
 CC The peptides are also useful for treating a patient suffering from
 CC bacterial, viral, fungal or other infection. The theta defensins have
 CC high antimicrobial activity and low haemolytic activity. The present
 CC sequence represents the rhesus monkey wild-type theta defensin RTD-1.
 XX Sequence 18 AA;
 SQ Query Match 87.1%; Score 101; DB 8; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00032;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GFCRCICTRGFCRCICTR 18
 Db 1 GFCRCICTRGFCRCICTR 18
 RESULT 13
 ADO35238
 ID ADO35238 standard; peptide; 18 AA.
 XX ADO35238;
 AC ADO35238;
 XX 15-JUL-2004 (first entry)
 DT Rhesus theta defensin analogue peptide arTD-1-OH.
 DE Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial;
 XX antiinflammatory; antibacterial; virucide; fungicide; food;
 KW contact lens solution; eye wash solution; inflammatory response;
 KW microbicidal inhibition; microbiostatic growth inhibition; disinfectant;
 KW food preservative; bacterial infection; viral infection;
 KW fungal infection; haemolytic activity.
 OS Macaca mulatta.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Disulfide-bond 3..16
 FT Disulfide-bond 5..14
 FT Disulfide-bond 7..12
 FT Modified-site 18
 FT /note= "Hydroxylated"

XX US2004014669-A1.
 XX 22-JAN-2004.
 XX 30-APR-2003; 2003US-00427715.
 XX 30-APR-2002; 2002US-0377071P.
 XX (REGC) UNIV CALIFORNIA.
 XX Selsted ME, Tran DQ;
 FI WPI; 2004-167945/16.
 DR Novel theta defensin analog useful for reducing or inhibiting growth or
 XX survival of a microorganism in an environment such as food or food
 XX product, contact lens solution, or eye wash solution, an inanimate
 XX object.
 XX Example 2; SEQ ID NO 12; 46pp; English.
 XX The invention relates to a theta defensin analogue defined by formulae
 CC detailed in the claims or appearing as ADO35239-ADO35257. The theta
 CC defensin analogue is useful for reducing or inhibiting growth or survival
 CC of a microorganism in an environment capable of sustaining the growth or
 CC survival of the microorganism and is useful for reducing or inhibiting
 CC growth or survival of a microorganism in an environment such as food or
 CC food product, a solution (e.g., contact lens solution, or eye wash
 CC solution), an inanimate object comprising surface, or a mammal. The
 CC peptides are also useful for decreasing inflammatory response and for
 CC microbicidal inhibition of survival of microorganism as well as
 CC microbiostatic inhibition of growth. Thus the peptides are useful as
 CC therapeutic agents, disinfectants, food preservatives, or medicaments.
 CC The peptides are also useful for treating a patient suffering from
 CC bacterial, viral, fungal or other infection. The theta defensins have
 CC high antimicrobial activity and low haemolytic activity. The present
 CC sequence represents a Rhesus theta defensin analogue peptide.
 XX Sequence 18 AA;
 SQ Query Match 87.1%; Score 101; DB 8; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00032;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GFCRCICTRGFCRCICTR 18
 Db 1 GFCRCICTRGFCRCICTR 18
 RESULT 14
 ADO35239
 ID ADO35239 standard; peptide; 18 AA.
 XX ADO35239;
 AC ADO35239;
 XX 15-JUL-2004 (first entry)
 DT Rhesus theta defensin analogue peptide arTD-1-NH.
 DE Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial;
 XX antiinflammatory; antibacterial; virucide; fungicide; food;
 KW contact lens solution; eye wash solution; inflammatory response;
 KW microbicidal inhibition; microbiostatic growth inhibition; disinfectant;
 KW food preservative; bacterial infection; viral infection;
 KW fungal infection; haemolytic activity.
 OS Macaca mulatta.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Disulfide-bond 3..16
 FT Disulfide-bond 5..14
 FT Disulfide-bond 7..12
 FT Modified-site 18
 FT /note= "Hydroxylated"

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FT Disulfide-bond 7. .12
FT Modified-site 18
FT /note= "Amidated"
XX
XX
XX
XX US2004014669-A1.
XX
XX 22-JAN-2004.
XX
XX 30-APR-2003; 2003US-00427715.
XX
XX 30-APR-2002; 2002US-0377071P.
XX (REGC ) UNIV CALIFORNIA.
XX
XX Selsted ME, Tran DQ;
XX WPI; 2004-167945/16.
XX
XX Novel theta defensin analog useful for reducing or inhibiting growth or
XX survival of a microorganism in an environment such as food or food
XX product, contact lens solution, or eye wash solution, an inanimate
XX object.
XX
XX Claim 1; SEQ ID NO 13; 46pp; English.
XX
XX The invention relates to a theta defensin analogue defined by formulae
XX detailed in the claims or appearing as ADO35239-ADO35257. The theta
XX defensin analogue is useful for reducing or inhibiting growth or survival
XX of a microorganism in an environment capable of sustaining the growth or
XX survival of the microorganism and is useful for reducing or inhibiting
XX growth or survival of a microorganism in an environment such as food or
XX food product, a solution (e.g., contact lens solution, or eye wash
XX solution), an inanimate object comprising surface, or a mammal. The
XX peptides are also useful for decreasing inflammatory response and for
XX microbicidal inhibition of survival of microorganism as well as
XX microbistatic inhibition of growth. Thus the peptides are useful as
XX therapeutic agents, disinfectants, food preservatives, or medicaments.
XX The peptides are also useful for treating a patient suffering from
XX bacterial, viral, fungal or other infection. The theta defensins have
XX high antimicrobial activity and low haemolytic activity. The present
XX sequence represents a Rhesus theta defensin analogue peptide.
XX
XX Sequence 18 AA;
XX
XX Query Match 87.1%; Score 101; DB 8; Length 18;
XX Best Local Similarity 83.3%; Pred. No. 0.00032;
XX Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 GFCRCICTRGFCRCICTR 18
XX
XX Db 1 GFCRCICTRGFCRCICTR 18
XX
XX
XX RESULT 15
XX ADO35250
XX ID ADO35250 standard; peptide; 18 AA.
XX
XX AC ADO35250;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX DE Rhesus theta defensin analogue peptide RTD-1-26.
XX
XX KW Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial;
XX antiinflammatory; antibacterial; virucide; fungicide; food;
XX contact lens solution; eye wash solution; inflammatory response;
XX microbicidal inhibition; microbistatic growth inhibition; disinfectant;
XX food preservative; bacterial infection; viral infection;
XX fungal infection; haemolytic activity; cyclic.
XX
XX OS Macaca mulatta.
XX
XX OS Synthetic.
XX

```

```

PH Key Location/Qualifiers
FT Modified-site 1. .18
FT /note= "The peptide is cyclised by a covalent link
FT between these two residues"
FT
FT Disulfide-bond 3. .16
FT Disulfide-bond 5. .14
FT Disulfide-bond 7. .12
XX
XX US2004014669-A1.
XX
XX 22-JAN-2004.
XX
XX 30-APR-2003; 2003US-00427715.
XX
XX 30-APR-2002; 2002US-0377071P.
XX (REGC ) UNIV CALIFORNIA.
XX
XX Selsted ME, Tran DQ;
XX WPI; 2004-167945/16.
XX
XX Novel theta defensin analog useful for reducing or inhibiting growth or
XX survival of a microorganism in an environment such as food or food
XX product, contact lens solution, or eye wash solution, an inanimate
XX object.
XX
XX Claim 1; SEQ ID NO 24; 46pp; English.
XX
XX The invention relates to a theta defensin analogue defined by formulae
XX detailed in the claims or appearing as ADO35239-ADO35257. The theta
XX defensin analogue is useful for reducing or inhibiting growth or survival
XX of a microorganism in an environment capable of sustaining the growth or
XX survival of the microorganism and is useful for reducing or inhibiting
XX growth or survival of a microorganism in an environment such as food or
XX food product, a solution (e.g., contact lens solution, or eye wash
XX solution), an inanimate object comprising surface, or a mammal. The
XX peptides are also useful for decreasing inflammatory response and for
XX microbicidal inhibition of survival of microorganism as well as
XX microbistatic inhibition of growth. Thus the peptides are useful as
XX therapeutic agents, disinfectants, food preservatives, or medicaments.
XX The peptides are also useful for treating a patient suffering from
XX bacterial, viral, fungal or other infection. The theta defensins have
XX high antimicrobial activity and low haemolytic activity. The present
XX sequence represents a Rhesus theta defensin analogue peptide.
XX
XX Sequence 18 AA;
XX
XX Query Match 87.1%; Score 101; DB 8; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 0.00032;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2005, 14:12:37 ; Search time 30 Seconds
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44.789 Million cell updates/sec

Title: US-10-009-317A-32

Perfect score: 116

Sequence: 1 GFCRCICTRGFCRCICTR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	87.1	18	3 US-09-309-487-1	Sequence 1, Appli
2	101	87.1	18	4 US-09-967-808-1	Sequence 1, Appli
3	93	80.2	18	4 US-10-141-645-5	Sequence 5, Appli
4	93	80.2	18	4 US-10-141-645-6	Sequence 6, Appli
5	91	78.4	18	3 US-09-309-487-9	Sequence 9, Appli
6	91	78.4	18	4 US-09-967-808-9	Sequence 9, Appli
7	90	77.6	18	4 US-10-141-645-1	Sequence 1, Appli
8	87	75.0	18	4 US-09-917-340-53	Sequence 53, Appli
9	87	75.0	18	4 US-10-141-645-2	Sequence 2, Appli
10	85	73.3	18	4 US-10-141-645-3	Sequence 3, Appli
11	85	73.3	18	4 US-10-141-645-4	Sequence 4, Appli
12	83	71.6	18	4 US-10-141-645-7	Sequence 7, Appli
13	75	64.7	18	4 US-10-141-645-8	Sequence 8, Appli
14	75	64.7	18	4 US-10-141-645-9	Sequence 9, Appli
15	73	62.9	92	3 US-09-309-487-21	Sequence 21, Appli
16	73	62.9	92	4 US-09-967-808-21	Sequence 21, Appli
17	64	55.2	76	3 US-09-309-487-14	Sequence 14, Appli
18	64	55.2	76	3 US-09-309-487-29	Sequence 29, Appli
19	64	55.2	76	4 US-09-967-808-14	Sequence 14, Appli
20	64	55.2	76	4 US-09-967-808-29	Sequence 29, Appli
21	64	55.2	76	4 US-10-141-645-15	Sequence 15, Appli
22	60	51.7	180	4 US-09-510-238A-286	Sequence 286, App
23	58	50.0	9	3 US-09-309-487-18	Sequence 18, Appli
24	58	50.0	9	4 US-09-967-808-18	Sequence 18, Appli
25	58	50.0	9	4 US-10-141-645-36	Sequence 36, Appli
26	56	48.3	9	4 US-10-141-645-49	Sequence 49, Appli
27	56	48.3	323	4 US-09-270-767-41896	Sequence 41896, A

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28 55.5 47.8 1400 3 US-08-630-915A-37 Sequence 37, Appli
29 55.5 47.8 1400 4 US-09-879-957-37 Sequence 37, Appli
30 55 47.4 168 4 US-09-252-991A-32502 Sequence 32502, A
31 55 47.4 585 4 US-09-252-991A-32321 Sequence 32321, A
32 55 47.4 2732 4 US-09-086-436-30 Sequence 30, Appli
33 54.5 47.0 801 1 US-07-906-349A-6 Sequence 6, Appli
34 54 46.6 18 3 US-09-604-864-8 Sequence 8, Appli
35 54 46.6 18 3 US-09-604-864-9 Sequence 9, Appli
36 54 46.6 18 4 US-10-042-872-8 Sequence 8, Appli
37 54 46.6 18 4 US-10-042-872-9 Sequence 9, Appli
38 53.5 46.1 1917 4 US-09-627-650B-5 Sequence 5, Appli
39 53.5 46.1 1917 4 US-09-436-063C-5 Sequence 5, Appli
40 53 45.7 1652 4 US-09-627-650B-1 Sequence 1, Appli
41 53 45.7 1652 4 US-09-436-063C-1 Sequence 1, Appli
42 53 45.7 2508 4 US-09-627-650B-7 Sequence 7, Appli
43 53 45.7 2508 4 US-09-436-063C-7 Sequence 7, Appli
44 53 45.7 2544 4 US-09-627-650B-3 Sequence 3, Appli
45 53 45.7 2544 4 US-09-436-063C-3 Sequence 3, Appli

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ALIGNMENTS

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RESULT 1
US-09-309-487-1
; Sequence 1, Application US/09309487
; Patent No. 6335318
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/309,487
; CURRENT FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-309-487-1

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Query Match      87.1%; Score 101; DB 3; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GFCRCICTRGFCRCICTR 18
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RESULT 2
US-09-967-808-1
; Sequence 1, Application US/09967808
; Patent No. 6514727
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/967,808
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US/09/309,487
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18

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Db 3 GFCRCLCRRGVCRCIC 18
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RESULT 7
US-10-141-645-1
; Sequence 1, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-141-645-1

Query Match 77.6%; Score 90; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 0.00023;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GFCRCICTRGFCRCICTR 18
| | | | | : | | | | |
Db 1 GICRCICGRCICRCICGR 18

RESULT 8
US-09-917-340-53
; Sequence 53, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-917-340-53

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RESULT 9
US-10-141-645-2
; Sequence 2, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-2

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Best Local Similarity 72.2%; Pred. No. 0.00051;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Db 1 GICRCICGRCICRCICGR 18

RESULT 10
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; Sequence 3, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-3

Query Match 73.3%; Score 85; DB 4; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.00085;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1 GICRCICGRCICRCICGR 18

Qy 1 GFCRCITRGFCRCICTR 18

Db 1 GICICGRCGICVCGR 18

RESULT 15
 US-09-309-487-21
 ; Sequence 21, Application US/09309487
 ; Patent No. 635318
 ; GENERAL INFORMATION:
 ; APPLICANT: Selsted, Michael E.
 ; APPLICANT: Tang, Yi-Quan
 ; APPLICANT: Yuan, Jun
 ; APPLICANT: Ouellette, Andre J.
 ; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
 ; FILE REFERENCE: P-UC 3095
 ; CURRENT APPLICATION NUMBER: US/09/309,487
 ; CURRENT FILING DATE: 1999-05-10
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 21
 ; LENGTH: 92
 ; TYPE: PRT
 ; ORGANISM: Macaca mulatta
 US-09-309-487-21

Query Match 62.9%; Score 73; DB 3; Length 92;
 Best Local Similarity 84.6%; Pred. NO. 0.067;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RCICTRGRCRCIC 16
 Db 65 RCICTRGRCRLLC 77

Search completed: April 28, 2005, 14:23:42
 Job time : 31 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2005, 14:13:43 ; Search time 91 Seconds
(without alignments)
65.889 Million cell updates/sec

Title: US-10-009-317A-32

Perfect score: 116

Sequence: 1 GFCRCICRGCRCICTR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	116	100.0	18	14	US-10-060-102-28
2	116	100.0	18	15	US-10-427-715-2
3	116	100.0	18	15	US-10-427-715-14
4	116	100.0	18	15	US-10-721-839-28
5	103	88.8	18	14	US-10-060-102-32
6	103	88.8	18	15	US-10-721-839-32
7	101	87.1	18	14	US-10-060-102-30
8	101	87.1	18	14	US-10-313-994-1
9	101	87.1	18	15	US-10-427-715-1
10	101	87.1	18	15	US-10-427-715-12
11	101	87.1	18	15	US-10-427-715-13
12	101	87.1	18	15	US-10-427-715-24
13	101	87.1	18	15	US-10-721-839-30

14	100	86.2	18	15	US-10-427-715-29	Sequence 29, Appl
15	93	80.2	18	14	US-10-141-645-5	Sequence 5, Appl
16	93	80.2	18	14	US-10-141-645-6	Sequence 6, Appl
17	91	78.4	18	14	US-10-313-994-9	Sequence 9, Appl
18	90	77.6	18	14	US-10-060-102-27	Sequence 27, Appl
19	90	77.6	18	14	US-10-141-645-1	Sequence 1, Appl
20	90	77.6	18	15	US-10-721-839-27	Sequence 27, Appl
21	89	76.7	18	15	US-10-427-715-23	Sequence 23, Appl
22	88	75.9	18	14	US-10-060-102-31	Sequence 31, Appl
23	88	75.9	18	15	US-10-721-839-31	Sequence 31, Appl
24	87	75.0	18	9	US-09-917-340-53	Sequence 53, Appl
25	87	75.0	18	14	US-10-141-645-2	Sequence 2, Appl
26	87	75.0	18	17	US-10-844-837-53	Sequence 53, Appl
27	87	75.0	18	17	US-10-909-119-67	Sequence 67, Appl
28	86	74.1	18	14	US-10-060-102-29	Sequence 29, Appl
29	86	74.1	18	15	US-10-427-715-3	Sequence 3, Appl
30	86	74.1	18	15	US-10-427-715-15	Sequence 15, Appl
31	86	74.1	18	15	US-10-427-715-16	Sequence 16, Appl
32	86	74.1	18	15	US-10-721-839-29	Sequence 29, Appl
33	85	73.3	18	14	US-10-141-645-4	Sequence 4, Appl
34	85	73.3	18	14	US-10-141-645-4	Sequence 4, Appl
35	85	73.3	18	15	US-10-427-715-30	Sequence 30, Appl
36	83	71.6	18	14	US-10-141-645-7	Sequence 7, Appl
37	83	71.6	18	15	US-10-427-715-19	Sequence 19, Appl
38	83	71.6	18	15	US-10-427-715-20	Sequence 20, Appl
39	82	70.7	18	15	US-10-427-715-17	Sequence 17, Appl
40	82	70.7	18	15	US-10-427-715-31	Sequence 31, Appl
41	75	64.7	18	14	US-10-141-645-8	Sequence 8, Appl
42	75	64.7	18	14	US-10-141-645-9	Sequence 9, Appl
43	74	63.8	18	15	US-10-427-715-28	Sequence 28, Appl
44	73	62.9	18	15	US-10-427-715-37	Sequence 37, Appl
45	73	62.9	18	15	US-10-427-715-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-10-060-102-28
; Sequence 28, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL CATHELICIDINS
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 28
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-060-102-28

Not for Art (NPA)

Query Match 100.0%; Score 116; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-06; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;
QY 1 GFCRCICRGCRCICTR 18

Db 1 GFCRCICTRGFCRCICTR 18
|||||

RESULT 2

US-10-427-715-2
; Sequence 2, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Thereof, and Methods of Use
; FILE REFERENCE: 66778-302(UC5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-427-715-2

Query Match 100.0%; Score 116; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICTR 18
|||||

Db 1 GFCRCICTRGFCRCICTR 18
|||||

RESULT 3

US-10-427-715-14
; Sequence 14, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Thereof, and Methods of Use
; FILE REFERENCE: 66778-302(UC5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-427-715-14

Query Match 100.0%; Score 116; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICTR 18
|||||

Db 1 GFCRCICTRGFCRCICTR 18
|||||

RESULT 4

US-10-721-839-28
; Sequence 28, Application US/10721839
; Publication No. US20040086535A1
; GENERAL INFORMATION:

; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
; TITLE OF INVENTION: CATHELICIDINS
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/721,839
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-721-839-28

Query Match 100.0%; Score 116; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICTR 18
|||||

Db 1 GFCRCICTRGFCRCICTR 18
|||||

RESULT 5

US-10-060-102-32
; Sequence 32, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
; TITLE OF INVENTION: CATHELICIDINS
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-060-102-32

Query Match 88.8%; Score 103; DB 14; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.9e-05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICTR 18

Db 1 GICRCICTRGFCRCICGR 18
| | | | | | | | | | | | | | | | | |

RESULT 6
US-10-721-839-32
; Sequence 32, Application US/10721839
; Publication No. US20040086535A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN CATHELICIDINS
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/721,839
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-721-839-32

Query Match 88.8%; Score 103; DB 15; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.9e-05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICTR 18
| | | | | | | | | | | | | | | | | |
Db 1 GICRCICTRGFCRCICGR 18

RESULT 7
US-10-060-102-30
; Sequence 30, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN CATHELICIDINS
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

NPA

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-060-102-30

Query Match 87.1%; Score 101; DB 14; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.9e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GFCRCICTRGFCRCICTR 18
| | | | | | | | | | | | | | | | | |
Db 1 GFCRCICRRGVCRICCTR 18

RESULT 8
US-10-313-994-1
; Sequence 1, Application US/10313994
; Publication No. US20030162718A1
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/10/313,994
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: US/09/309,487
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-313-994-1

Query Match 87.1%; Score 101; DB 14; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.9e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICTR 18
| | | | | | | | | | | | | | | | | |
Db 1 GFCRCICRRGVCRICCTR 18

RESULT 9
US-10-427-715-1
; Sequence 1, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Thereof, and Methods of Use
; FILE REFERENCE: 66778-302(UCS754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-427-715-1

Query Match 87.1%; Score 101; DB 15; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.9e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICTR 18
| | | | | | | | | | | | | | | | | |

Db 1 GFCRCCLCRGVCRICCTR 18

RESULT 10

US-10-427-715-12
 ; Sequence 12, Application US/10427715
 ; Publication No. US20040014669A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Selsted, Michael E.
 ; APPLICANT: Tran, Dat Q.
 ; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
 ; TITLE OF INVENTION: Thereof, and Methods of Use
 ; FILE REFERENCE: 66778-302(UC5754)
 ; CURRENT APPLICATION NUMBER: US/10/427,715
 ; CURRENT FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: US 60/377,071
 ; PRIOR FILING DATE: 2002-04-30
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic construct
 US-10-427-715-12

Query Match 87.1%; Score 101; DB 15; Length 18;
 Best Local Similarity 83.3%; Pred. No. 4.9e-05;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICCTR 18

Db 1 GFCRCCLCRGVCRICCTR 18

RESULT 11

US-10-427-715-13
 ; Sequence 13, Application US/10427715
 ; Publication No. US20040014669A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Selsted, Michael E.
 ; APPLICANT: Tran, Dat Q.
 ; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
 ; TITLE OF INVENTION: Thereof, and Methods of Use
 ; FILE REFERENCE: 66778-302(UC5754)
 ; CURRENT APPLICATION NUMBER: US/10/427,715
 ; CURRENT FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: US 60/377,071
 ; PRIOR FILING DATE: 2002-04-30
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic construct
 ; FEATURE:
 ; NAME/KEY: AMIDATION
 ; LOCATION: 18
 ; OTHER INFORMATION: at the C terminus
 US-10-427-715-13

Query Match 87.1%; Score 101; DB 15; Length 18;
 Best Local Similarity 83.3%; Pred. No. 4.9e-05;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICCTR 18

Db 1 GFCRCCLCRGVCRICCTR 18

RESULT 12

US-10-427-715-24
 ; Sequence 24, Application US/10427715
 ; Publication No. US20040014669A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Selsted, Michael E.
 ; APPLICANT: Tran, Dat Q.
 ; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
 ; TITLE OF INVENTION: Thereof, and Methods of Use
 ; FILE REFERENCE: 66778-302(UC5754)
 ; CURRENT APPLICATION NUMBER: US/10/427,715
 ; CURRENT FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: US 60/377,071
 ; PRIOR FILING DATE: 2002-04-30
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic construct
 US-10-427-715-24

Query Match 87.1%; Score 101; DB 15; Length 18;
 Best Local Similarity 88.9%; Pred. No. 4.9e-05;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICCTR 18

Db 1 GFCRCRCRTRGFCRCICCTR 18

RESULT 13

US-10-721-839-30
 ; Sequence 30, Application US/10721839
 ; Publication No. US20040086535A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MAURY, WENDY
 ; APPLICANT: STAPLETON, JACK
 ; APPLICANT: ROLLER, RICHARD
 ; APPLICANT: STINSKI, MARK
 ; APPLICANT: MCCRAY, PAUL B.
 ; APPLICANT: TACK, BRIAN
 ; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
 ; TITLE OF INVENTION: CATHELICIDINS
 ; FILE REFERENCE: IOWA:035US
 ; CURRENT APPLICATION NUMBER: US/10/721,839
 ; CURRENT FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: US/10/060,102
 ; PRIOR FILING DATE: 2002-02-22
 ; PRIOR APPLICATION NUMBER: 60/309,368
 ; PRIOR FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: 60/265,270
 ; PRIOR FILING DATE: 2001-01-30
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 30
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 US-10-721-839-30

Query Match 87.1%; Score 101; DB 15; Length 18;
 Best Local Similarity 83.3%; Pred. No. 4.9e-05;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICCTR 18

Db 1 GFCRCCLCRGVCRICCTR 18

Job time : 91.5 secs

RESULT 14

US-10-427-715-29
; Sequence 29, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Selssted, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Thereof, and Methods of Use
; FILE REFERENCE: 66778-302(UC5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-427-715-29

Query Match 86.2%; Score 100; DB 15; Length 18;
Best Local Similarity 93.8%; Pred. No. 6.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCIC 16
| | | | | | | | | | | | | | | |
DB 1 GICRCICTRGFCRCIC 16

RESULT 15

US-10-141-645-5
; Sequence 5, Application US/10141645
; Publication No. US20030144184A1
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-5

Query Match 80.2%; Score 93; DB 14; Length 18;
Best Local Similarity 77.8%; Pred. No. 0.00039;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICTR 18
| | | | | | | | | | | | | | | |
DB 1 GYCRCICGRCICRCICGR 18

Search completed: April 28, 2005, 14:26:50

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OM protein - protein search, using sw model

Run on: April 28, 2005, 14:00:51 ; Search time 26 Seconds
(without alignments)
66.612 Million cell updates/sec

Title: US-10-009-317a-32

Perfect score: 116
Sequence: 1 GFCRCICTRGFCRCICTR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	87	75.0	18	2 C59089	theta defensin-1 -
2	64	55.2	76	2 A59089	theta defensin 1a
3	54.5	47.0	248	2 E71602	probable integral
4	54	46.6	290	2 G72858	AcOrf-70 protein -
5	53	45.7	164	2 T24272	hypothetical prote
6	53	45.7	188	2 T15651	hypothetical prote
7	52.5	45.3	73	2 JC1066	trypsin inhibitor
8	51	44.0	72	1 TIMB	trypsin inhibitor
9	51	44.0	419	2 S69207	vascular endotheli
10	50.5	43.5	83	2 S07405	proteinase inhibit
11	50.5	43.5	94	2 JC2225	Bowman-Birk protei
12	50.5	43.5	103	1 TISYC2	proteinase inhibit
13	50	43.1	624	1 S54581	probable membrane
14	49	42.2	152	2 T18975	hypothetical prote
15	49	42.2	157	2 A25964	thyroglobulin - ra
16	49	42.2	1700	2 S08167	Balbani ring 3 pr
17	48	41.4	72	1 T12B1P	proteinase inhibit
18	48	41.4	78	1 T12B1A	proteinase inhibit
19	48	41.4	79	1 T12B2	proteinase inhibit
20	48	41.4	83	2 S07941	proteinase inhibit
21	48	41.4	102	1 T1SYD2	proteinase inhibit
22	48	41.4	160	2 T25185	hypothetical prote
23	48	41.4	306	2 S32834	methyloviologen-red
24	48	41.4	476	2 JC5042	G protein-coupled
25	48	41.4	1353	1 JH0675	restrictin precurs
26	47.5	40.9	77	2 L48725	Q300 protein - mou
27	47.5	40.9	550	2 PQ0618	hypothetical prote
28	47	40.5	113	2 S56648	trypsin inhibitor
29	47	40.5	317	2 JC7597	chondromodulin-I 1

tenomodulin - mous
hypothetical prote
hypothetical prote
hypothetical prote
gp330 protein prec
hypothetical prote
related to mutanas
reelin precursor -
proteinase inhibit
hypothetical prote
hypothetical prote
latent transformin
unknown protein, 9
gene serrate prote
EF1 protein - fowl

ALIGNMENTS

RESULT 1

C59089
theta defensin-1 - rhesus macaque

N;Alternate names: RTD-1

C;Species: Macaca mulatta (rhesus macaque)

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: C59089

R;Tang, Y.Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.

Science 286, 498-502, 1999

A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation

A;Reference number: A59089; MUID:99453140; PMID:10521339

A;Accession: C59089

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 <SEL>

A;Note: this sequence is cyclically permuted by -6 residues from the sequence presented

C;Comment: For the two contributing precursor sequences, see PIR:A59089 and PIR:B59089.

C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing

F;1-9/Region: theta defensin 1a-derived

F;10-18/Region: theta defensin 1b-derived

F;1-18/Cross-link: cyclopeptide (Arg-Cys) #status experimental

F;2-11,4-9,13-18/Dsulfide bonds: #status experimental

F;9-10/Cross-link: cyclopeptide (Cys-Arg) #status experimental

Query Match 75.0%; Score 87; DB 2; Length 18;

Best Local Similarity 86.7%; Pred. No. 0.00014;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RCICTRGFCRCICTR 18

Db 1 RCICTRGFCRCICLRR 15

RESULT 2

A59089
theta defensin 1a precursor - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: A59089

R;Tang, Y.Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.

Science 286, 498-502, 1999

A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation

A;Reference number: A59089; MUID:99453140; PMID:10521339

A;Accession: A59089

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-76 <TAN>

A;Cross-references: UNIPROT:P82270; GB:AF191100; NID:G6137227; PIDN:AAF04389.1; PID:G61

C;Comment: For the complete mature sequence, see PIR:C59089.

C;Superfamily: mammalian defensin

C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-64/Domain: amino-terminal propeptide #status predicted <PRO>
F;74-76/Domain: carboxyl-terminal propeptide #status predicted <CP>

Query Match 55.2%; Score 64; DB 2; Length 76;
Best Local Similarity 83.3%; Pred. No. 0.2;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RCICTRGFCRCI 15
|||||
Db 65 RCICTRGFCRL 76

RESULT 3

E71602
Probable integral membrane protein PFB0950w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C;Accession: E71602
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: E71602
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-248 <CAR>
A;Cross-references: UNIPROT:O96282; GB:AE001428; GB:AE001362; NID:g3845316; PIDN:AAC7197
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0950w

Query Match 47.0%; Score 54.5; DB 2; Length 248;
Best Local Similarity 60.0%; Pred. No. 6;
Matches 9; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 3 CRCICTRGFCRCICT 17
|||||
Db 163 CSCICT---CTCICS 174

RESULT 4

G72858
AcOrf-70 protein - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, AcMPV
A;Note: dsDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Accession: G72858
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Perber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Accession: G72858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-290 <AYR>
A;Cross-references: UNIPROT:P41470; GB:L22858; NID:g510708; PIDN:AAA66700.1; PID:g559139
C;Genetics:
A;Gene: AcOrf-70

Query Match 46.6%; Score 54; DB 2; Length 290;
Best Local Similarity 40.9%; Pred. No. 7.7;
Matches 11; Conservative 2; Mismatches 4; Indels 10; Gaps 2;

QY 2 FRCICT-----RGF-CRCICTR 18
|||||
Db 218 FARCFCTNTWQCFCPRQYKCEICIR 244

RESULT 5

T24272
hypothetical protein T01B7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24272

R;Sims, M.

submitted to the EMBL Data Library, October 1995
A;Reference number: Z19867

A;Accession: T24272

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-164 <WIL>

A;Cross-references: UNIPROT:Q22048; EMBL:Z66499; PIDN:CAA91301.1; GSPDB:GN00020; CESP:T

A;Experimental source: clone T01B7

C;Genetics:

A;Gene: CESP:T01B7.8

A;Map position: 2

A;Introns: 20/3; 90/2

Query Match 45.7%; Score 53; DB 2; Length 164;

Best Local Similarity 50.0%; Pred. No. 6.9;

Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GFRCICTRGFCRCICTR 18
|||||
Db 80 GCGGCCCRPRCCCCRR 97

RESULT 6

T15651

hypothetical protein C27A2.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T15651

R;Nhan, M.

submitted to the EMBL Data Library, May 1996

A;Description: The sequence of C. elegans cosmid C27A2.

A;Reference number: Z18382

A;Accession: T15651

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-188 <NHA>

A;Cross-references: UNIPROT:Q18238; EMBL:U58760; NID:g1330384; PID:g1330389; PIDN:AAB00

A;Experimental source: strain Bristol N2; clone C27A2

C;Genetics:

A;Gene: CESP:C27A2.5

A;Map position: 2

A;Introns: 19/3; 91/2

Query Match 45.7%; Score 53; DB 2; Length 188;
Best Local Similarity 50.0%; Pred. No. 7.6;

Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GFRCICTRGFCRCICTR 18
|||||
Db 81 GCGGCCCRPRCCCCRR 98

RESULT 7

JC1066

trypsin inhibitor - mung bean

C;Species: Vigna radiata (mung bean)

C;Date: 02-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 18-Aug-2000

C;Accession: JC1066

R;Chen, C.Q.; Mao, J.F.; Zhang, M.F.; Dai, J.F.

Chinese J. Biotechnol. 9, 54-60, 1993

A;Title: Synthesis of mung bean trypsin inhibitor by the combination of the single str

A;Reference number: JC1066

A;Accession: JC1066

A;Molecule type: DNA

A;Residues: 1-73 <CHE>

C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology

C;Keywords: serine proteinase inhibitor

F;2-73/Product: trypsin inhibitor #status predicted <MAT>

F;14-40/Domain: Bowman-Birk inhibitor repeat homology <BB1>

F;41-66/Domain: Bowman-Birk inhibitor repeat homology <BB12>

Query Match 45.3%; Score 52.5; DB 2; Length 73;
 Best Local Similarity 48.0%; Pred. No. 4.6;
 Matches 12; Conservative 3; Mismatches 1; Indels 9; Gaps 3;
 QY 3 CR-CICTR---GFCRCI-----CTR 18
 DB 41 CKSCICTRSMKRCRLDTDDFCCK 65

RESULT 8
 TIMB
 trypsin inhibitor (Bowman-Birk) - mung bean
 C:Species: Vigna radiata (mung bean)
 C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
 C:Accession: A01301
 R:Zhang, Y.; Luo, S.; Tan, F.; Qi, Z.; Xu, L.; Zhang, A.
 Sci. Sin. 25, 268-277, 1982
 A:Title: Complete amino acid sequence of mung bean trypsin inhibitor.
 A:Reference number: A01301
 A:Accession: A01301
 A:Molecule type: protein
 A:Residues: 1-72 <2HA>
 A:CROSS-references: UNIPROT:P01062
 A:Note: three isoinhibitors are also found whose amino ends differ slightly from that of Lys-1, respectively
 C:Comment: This inhibitor stoichiometrically inhibits trypsin in a molar ratio of 1:2.
 C:Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
 C:Keywords: duplication; serine proteinase inhibitor
 F:13-39/Domain: Bowman-Birk inhibitor repeat homology <BB1>
 F:40-65/Domain: Bowman-Birk inhibitor repeat homology <BB2>
 F:12-66,13-28,16-62,18-26,36-43,40-55,45-53/Disulfide bonds: #status predicted
 F:20/Inhibitory site: Lys (trypsin) #status predicted
 F:47/Inhibitory site: Arg (trypsin) #status predicted

Query Match 44.0%; Score 51; DB 1; Length 72;
 Best Local Similarity 57.9%; Pred. No. 6.8;
 Matches 11; Conservative 2; Mismatches 2; Indels 4; Gaps 2;
 QY 3 CR-CICTR---GFCRCICT 17
 DB 40 CKSCICTRSMKRCRLDT 58

RESULT 9
 S69207
 vascular endothelial growth factor C precursor - human
 N:Alternate names: Flt4 ligand DHM
 C:Species: Homo sapiens (man)
 C>Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
 C:Accession: S69207; S61795; S71443; S69208; G02659
 R:Joukov, V.; Pajusola, K.; Kaipainen, A.; Chillov, D.; Lahtinen, I.; Kukkk, E.; Saksela, EMO J. 15, 1751, 1996
 A:Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand for VEGFR-2
 A:Reference number: S69207; MUID:96203094; PMID:8612600
 A:Accession: S69207
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-419 <JOU>
 A:CROSS-references: UNIPROT:P49767; EMBL:X94216; NID:g1177488; PIDN:CAA63907.1; PID:e221
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
 A:Note: only a part of the translation is shown
 A:Note: this is a revision to the sequence from reference S61795
 R:Joukov, V.; Pajusola, K.; Kaipainen, A.; Chillov, D.; Lahtinen, I.; Kukkk, E.; Saksela, EMO J. 15, 290-298, 1996
 A:Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (V) receptor
 A:Reference number: S61795; MUID:96178224; PMID:8617204
 A:Accession: S61795
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 70-419 <JOU1>
 A:Note: this sequence has been revised in reference S69207
 A:Accession: S71443

A:Molecule type: protein
 A:Residues: 'X',104-120 <JOU2>
 R:Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
 submitted to the EMBL Data Library, December 1995
 A:Description: Vascular endothelial growth factor related protein (VRP): A ligand and a
 A:Reference number: S69208
 A:Accession: S69208
 A:Molecule type: mRNA
 A:Residues: 1-419 <LEE>
 A:CROSS-references: EMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989
 R:Mortis, J.C.
 submitted to the EMBL Data Library, May 1996
 A:Reference number: H01557
 A:Accession: G02659
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-419 <MOR>
 A:CROSS-references: EMBL:U58111; NID:g1373426; PIDN:AAB02909.1; PID:g1373427
 C:Genetics:
 A:Gene: GDB:VEGFC; VRP
 A:CROSS-references: GDB:3890883; OMIM:601528
 F:1-12/Domain: signal sequence #status predicted <SIG>
 F:13-102/Domain: propeptide #status predicted <PRO>
 F:103-419/Product: vascular endothelial growth factor C #status experimental <MAT>

Query Match 44.0%; Score 51; DB 2; Length 419;
 Best Local Similarity 36.0%; Pred. No. 22;
 Matches 9; Conservative 2; Mismatches 4; Indels 10; Gaps 1;
 QY 3 CRCICTR-----GFCRCICT 17
 DB 339 CQCVCRTCPRNQPLNPGKACECT 363

RESULT 10
 S07405
 proteinase inhibitor (Bowman-Birk) C-II - soybean
 C:Species: Glycine max (soybean)
 C>Date: 02-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S07405; S29608; S40113
 R:Joudrier, P.E.; Foard, D.E.; Floener, L.A.; Larkins, B.A.
 Plant Mol. Biol. 10, 35-42, 1987
 A:Title: Isolation and sequence of cDNA encoding the soybean protease inhibitors PI IV
 A:Reference number: S07405
 A:Accession: S07405
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-83 <JOU>
 A:CROSS-references: UNIPROT:P01063; EMBL:M20732; NID:g169944; PIDN:AAA33953.1; PID:g169944
 A:Note: the sequences of codons 8-13 and 14-27 are interchanged in the authors' translation
 R:Baek, J.M.; Kim, S.I.
 submitted to the EMBL Data Library, October 1992
 A:Description: Nucleotide sequence of a cDNA encoding the soybean Bowman-Birk proteinase
 A:Reference number: S29559
 A:Accession: S29608
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-83 <BAE>
 A:CROSS-references: EMBL:X68705; NID:g18567; PIDN:CAA4856.1; PID:g18567
 R:Giordano, A.; DelleDonne, M.; Fogher, C.; Marchetti, S.
 submitted to the EMBL Data Library, December 1993
 A:Description: Nucleotide sequence encoding a soybean C-II proteinase inhibitor.
 A:Reference number: S40113
 A:Accession: S40113
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-83 <GIO>
 A:CROSS-references: EMBL:X76727; NID:g436413; PIDN:CAAS4144.1; PID:g436414
 C:Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
 C:Keywords: serine proteinase inhibitor
 F:22-48/Domain: Bowman-Birk inhibitor repeat homology <BB1>
 F:49-74/Domain: Bowman-Birk inhibitor repeat homology <BB12>

A:Gene: CBSP:C06A1.6
 A:Map position: 2
 A:Introns: 22/3

Query Match 42.2%; Score 49; DB 2; Length 152;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCIC 16
 | | | | | | | | | |
 Db 67 GCGCCCCCRPRCCCC 82

RESULT 15

A25964
 thyroglobulin - rat (fragments)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 20-Jun-1989 #sequence_revision 30-Jun-1991 #text_change 11-Apr-1997
 C:Accession: A25964
 R:Musci, A.M.; Avvedimento, E.V.; Polistina, C.; Ursini, V.M.; Obici, S.; Nitsch, L.; C
 Proc. Natl. Acad. Sci. U.S.A. 83, 323-327, 1986
 A:Title: The complete structure of the rat thyroglobulin gene.
 A:Reference number: A25964; MUID:86094383; PMID:3455768
 A:Accession: A25964
 A:Molecule type: DNA
 A:Residues: 1-157 <MUS>
 A:Cross-references: GB:M12558
 A>Note: the authors translated the codon GTG for residue 44 as Leu
 C:Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homol
 C:Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
 F:35-60/Domain: thyroglobulin type I repeat homology (fragment) <THY1>
 F:134-138/Domain: thyroglobulin type I repeat homology (fragment) <THY2>
 F:25/Modified site: thyroxine (Tyr) #status predicted

Query Match 42.2%; Score 49; DB 2; Length 157;
 Best Local Similarity 32.0%; Pred. No. 20;
 Matches 8; Conservative 4; Mismatches 5; Indels 8; Gaps 1;

QY 1 GFCRCIC-----TRGFCRCICT 17
 | | | | | | | | | |
 Db 110 GECWCVCSPFVPTCTSEGCYCVC 134

Search completed: April 28, 2005, 14:22:37
 Job time : 28 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2005, 13:58:25 ; Search time 114 Seconds
(without alignments)
80.855 Million cell updates/sec

Title: US-10-009-317A-32
Perfect score: 116
Sequence: 1 GFCRCICTRGFCRCICTR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	55.2	76	1 TD1A_MACMU	P82270 macaca mula
2	59	50.9	168	2 Q6P8T4	Q6p8t4 mus musculus
3	59	50.9	168	2 Q8CH20	Q8ch20 mus musculus
4	59	50.9	168	2 Q9D912	Q9d912 mus musculus
5	59	50.9	173	2 Q9DAK2	Q9dak2 mus musculus
6	59	50.9	274	2 Q94SG1	Q94sg1 oryza sativ
7	56.5	48.7	163	2 Q8VU20	Q8vj20 mycobacteri
8	56	48.3	937	2 Q9BLJ1	Q9blj1 ciona intes
9	54.5	47.0	307	2 Q96282	Q96282 plasmodium
10	54	46.6	290	1 Y070 NPVAC	P41470 autographa
11	54	46.6	991	2 Q7SEQ2	Q7seq2 neurospora
12	53.5	46.1	174	2 Q9NRB6	Q9nr66 homo sapien
13	53	45.7	164	2 Q22048	Q22048 caenorhabdi
14	53	45.7	166	2 Q95QY1	Q95qy1 caenorhabdi
15	53	45.7	187	2 Q18238	Q18238 caenorhabdi
16	53	45.7	197	2 Q17641	Q17641 caenorhabdi
17	53	45.7	602	2 Q75NZ5	Q75nz5 chlamydomon
18	53	45.7	1365	2 Q75N88	Q75n88 homo sapien
19	53	45.7	2871	2 Q75N87	Q75n87 homo sapien
20	52.5	45.3	129	2 Q7RU70	Q7ru70 anopheles g
21	52.5	45.3	273	2 Q94U26	Q94uz6 leishmania
22	52.5	45.3	512	2 Q6RY99	Q6ry99 rattus norv
23	52	44.8	66	2 Q9PYQ3	Q9pyq3 xestia c-ni
24	52	44.8	146	2 Q7QBV4	Q7qbv4 anopheles g
25	52	44.8	161	2 Q8MZ55	Q8mz55 drosophila
26	52	44.8	1823	2 Q7PRP5	Q7prp5 anopheles g
27	51.5	44.4	190	2 Q9UI23	Q9ui23 homo sapien
28	51	44.0	59	2 Q6IG37	Q6ig37 drosophila
29	51	44.0	72	1 IBB_PHAU	P01062 phaseolus a
30	51	44.0	201	2 Q6ZQS2	Q6zqs2 homo sapien
31	51	44.0	326	2 Q91ZHE	Q91zh6 meriones un

32	51	44.0	336	2	Q7PVN9	Q7pvn9 anopheles g
33	51	44.0	415	1	VEGC MOUSE	P97953 mus musculu
34	51	44.0	415	2	Q91ZE3	Q91ze3 rattus norv
35	51	44.0	419	1	VEGC_HUMAN	P49767 homo sapien
36	51	44.0	482	2	Q6A1N6	Q6a1n6 euplotes va
37	50.5	43.5	83	1	IBB2 SOYBN	P01063 glycine max
38	50.5	43.5	91	2	Q8LC92	Q8lc92 arabidopsis
39	50.5	43.5	109	2	Q8RU22	Q8ru22 glycine soj
40	50.5	43.5	168	2	Q87BL8	Q87bl8 xylella fas
41	50.5	43.5	222	2	Q6VZ23	Q6vz23 canarypox v
42	50.5	43.5	379	2	Q7SXV0	Q7sxv0 brachydanio
43	50.5	43.5	1411	2	Q7S1G4	Q7s1g4 neurospora
44	50	43.1	66	2	Q9AVA3	Q9ava3 pisum sativ
45	50	43.1	212	2	Q7YVW7	Q7yvw7 caenorhabdi

ALIGNMENTS

RESULT 1

TD1A_MACMU STANDARD; PRT; 76 AA.
AC P82270: Q9TU01;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Theta defensin-1, subunit A precursor (RTD-1a) (Demidefensin 2).
OS Name=RTD1A;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A. SEQUENCE OF 65-73. TISSUE SPECIFICITY,
RP DEVELOPMENTAL STAGE, AND DISULFIDE BONDS.
RC TISSUE=Bone marrow, and Leukocyte;
RX MEDLINE=94453140; PubMed=10521339; DOI=10.1126/science.286.5439.498;
RA Tang Y.-Q., Yuan J., Oesapay G., Oesapay K., Tran D., Miller C.J.,
RA Ouellette A.J., Selsted M.E.;
RT 'A cyclic antimicrobial peptide produced in primate leukocytes by the
RT ligation of two truncated alpha-defensins.';
RL Science 286:498-502(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Zhao C., Nguyen T., Lehrer R.I.;
RT 'CDNA cloning of three alpha-defensins and three demidefensins from
RL rhesus monkey bone marrow.';
CC Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Active against the Gram-positive bacteria S.aureus and
CC L.monocytogenes, Gram-negative bacteria S.typhimurium and E.coli
CC ML35 and fungi C.albicans and C.neoformans in vitro.
CC -!- SUBUNIT: Forms a cyclic heterodimer composed of subunits A and B;
CC disulfide-linked.
CC -!- TISSUE SPECIFICITY: Expressed in bone marrow. Detected in
CC promyelocytes, myelocytes and mature neutrophils and monocytes.
CC -!- DEVELOPMENTAL STAGE: Expression begins early during granulocyte
CC myelopoiesis.
CC -!- PTM: This is a cyclic peptide.
CC -!- SIMILARITY: Belongs to the corticostatin/defensin family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF191100; AAF04389.1; -;
CC EMBL; AF191102; AAF04391.1; -;
CC EMBL; AF184157; AAF07924.1; -;

DR PIR; A59089; A59089.
 DR InterPro: IPR002366; Defensin_propep.
 DR Pfam: PF00879; Defensin_propep; 1.
 DR PROSITE; PS00269; DEFENSIN; FALSE NEG.
 KW Antibiotic; Defensin; Direct protein sequencing; Fungicide; Signal.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 64
 FT PEPTIDE 65 73 Theta defensin-1, subunit A.
 FT PROPEP 74 76
 FT DISULFID 66 66 Interchain (with C-66 of subunit B).
 FT DISULFID 68 73
 FT CONFLICT 38 38 T -> A (in Ref. 2).
 FT SEQUENCE 76 AA; 8242 MW; BEA207932A030590 CRC64;
 SQ
 Query Match 55.2%; Score 64; DB 1; Length 76;
 Best Local Similarity 83.3%; Pred. No. 0.34;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 RCICTRGFCRCI 15
 DB 65 RCICTRGFCRL 76
 RESULT 2
 Q6P8T4 PRELIMINARY; PRT; 168 AA.
 ID Q6P8T4
 AC Q6P8T4
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE 4931420D14Rik protein.
 GN Name=4931420D14Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Xu X., Bai X., Silvius D., Escalier D., McFarland L., Xu P.-X.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF463502; AAO15675.1; -
 DR MGD; MGI:1913992; 4931420D14Rik.
 SQ SEQUENCE 168 AA; 18957 MW; 8F30D3D27B9BF595 CRC64;
 Query Match 50.9%; Score 59; DB 2; Length 168;
 Best Local Similarity 56.2%; Pred. No. 2.9;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 3 RCICTRGFCRCICTR 18
 DB 66 CRCCVCRCRCRCSR 81
 RESULT 4
 Q9D9I2 PRELIMINARY; PRT; 168 AA.
 ID Q9D9I2
 AC Q9D9I2
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 DE library, clone1700065I05 product:hypothetical Cysteine-rich region
 DE containing protein, full insert sequence.
 GN Name=4931420D14Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RC Carninci P., Hayashizaki Y.;
 RA Carninci P., Hayashizaki Y.;
 RT "high-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RC RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The FANTOM Consortium.
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 QY 3 RCICTRGFCRCICTR 18

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein C1SERIPDM.
GN Name=C1SERIPDM;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21329048; PubMed=11435398; DOI=10.1101/gr.GR-1617R;
RA Mayer K., Murphy G., Tarchini R., Wambutt R., Volkert G., Pohl T.,
RA Duesterhoeft A., Stiekema W., Entian K.D., Terry N., Lemcke K.,
RA Haase D., Hall C.R., van Dodeleerd A.M., Tingey S.V., Newes H.W.,
RA Bevan M., Bancroft I.;
RT "Conservation of microstructure between a sequenced region of the
RT genome of rice and multiple segments of the genome of Arabidopsis
RT thaliana.";
RL Genome Res; 11:1167-1174(2001).
DR EMBL; AJ307662; CAC39030.1; -;
DR Gramene; Q949G1; -;
KW Hypothetical protein.
SQ SEQUENCE 274 AA; 28657 MW; AB547D9BD5470AE1 CRC64;
Query Match 50.9%; Score 59; DB 2; Length 274;
Best Local Similarity 66.7%; Pred. No. 4.3; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 5;
QY 4 RCICTRGFCRCICTR 18
DB 185 RCCHRGCCRCRATR 199
RESULT 7
Q8VJ20 PRELIMINARY; PRT; 163 AA.
ID Q8VJ20
AC Q8VJ20
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MT3454;
OS Mycobacterium tuberculosis
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Uterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains";
RL J. Bacteriol. 184:5479-5490(2002).
DR EMBL; AE000516; AAK47795.1; -;
DR TIGR; MT3454; -;
KW Hypothetical protein.
SQ SEQUENCE 163 AA; 18621 MW; B5E62AB951B2AC3C CRC64;
Query Match 48.7%; Score 56.5; DB 2; Length 163;
Best Local Similarity 60.0%; Pred. No. 5.8; Indels 1; Gaps 1;
Matches 9; Conservative 3; Mismatches 2;
QY 3 RCICTR-GFCRCIC 16
DB 137 CRHVCTRGVGRVLC 151

RESULT 8
Q9BLJ1 PRELIMINARY; PRT; 937 AA.
ID Q9BLJ1
AC Q9BLJ1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ci-METAL.
GN Name=Ci-metal;
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21347414; PubMed=11455433;
RA Nakayama A., Satoh Y., Satoh N.;
RT "Isolation and characterization of genes that are expressed during
RT Ciona intestinalis metamorphosis.";
RL Dev. Genes Evol. 211:184-189(2001).
DR HSSP; AB041857; BAB40596.1; -;
DR HSSP; P00743; ICCF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001212; Somatomedin B.
DR InterPro; IPR001491; Thrombomodulin.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF07645; EGF CA; 14.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PRINTS; PR00907; THROMBOMODULN.
DR SMART; SM00179; EGF CA; 14.
DR PROSITE; PS00010; ASX_HYDROXYL; 14.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 19.
DR PROSITE; PS00026; EGF_3; 19.
DR PROSITE; PS01187; EGF CA; 12.
DR PROSITE; PS00524; SMB_1; 1.
DR EGF-like domain.
KW EGF-like domain.
SQ SEQUENCE 937 AA; 101043 MW; 8C57830C8E391D07 CRC64;
Query Match 48.3%; Score 56; DB 2; Length 937;
Best Local Similarity 58.8%; Pred. No. 29;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 GFCRCICTRGFCRCIC 17
DB 552 GSYRCICARGFGSLCT 568
RESULT 9
O96282 PRELIMINARY; PRT; 307 AA.
ID O96282
AC O96282;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein PFB0950W.
GN Name=PFB0950W;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=99021743; PubMed=9804551; DOI=10.1126/science.282.5391.1126;
RX Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
RA Koonin E.V., Shalloom S., Mason T., Yu K., Fujii C., Pederson J.,

RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RL falciparum.";
RN Science 282:1126-1132(1998).
RP [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft B., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
RL EMBL; AE001428; AAC71979.2; -
DR PIR; E71602; E71602.
DR HSPP; P01056; IH34.
DR InterPro; IPR001368; TNFR_C6.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 307 AA; 35537 MW; B95A3DB354D4BE71 CRC64;
Query Match 47.0%; Score 54.5; DB 2; Length 307;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
QY 3 CRCICTRGFCRCICT 17
DB 222 CSCICT---CTCICS 233
RESULT 10
Y070 NPVAC STANDARD; PRT; 290 AA.
AC P41470;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE Hypothetical 34.4 kDa protein in LEF3-TAP2 intergenic region.
OS Autographa californica nuclear polyhedrosis virus (AcMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=46015;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C6;
RX MEDLINE=94303173; PubMed=8030224;
RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
RT "The complete DNA sequence of Autographa californica nuclear
RL polyhedrosis virus.";
RL Virology 202:586-605(1994).
CC
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CC
CC EMBL; L22858; AAA66700.1; -
DR PIR; G72858;
DR InterPro; IPR000519; P_trefol.
KW Hypothetical protein.
SQ SEQUENCE 290 AA; 34408 MW; CA78BA9C8B5AB997 CRC64;

Query Match 46.6%; Score 54; DB 1; Length 290;
Best Local Similarity 40.7%; Pred. No. 19;
Matches 11; Conservative 2; Mismatches 4; Indels 10; Gaps 2;
QY 2 FCRICICT-----RGF-CRCICTR 18
DB 218 PARCFCTNTMQCFPCPGYKCEICRR 244
RESULT 11
Q7SEQ2 PRELIMINARY; PRT; 991 AA.
AC Q7SEQ2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Predicted protein.
DE Names=NCU02165.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehan B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Salizemnikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysysselis M., Maucelli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003)
CC
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABX01000029; EAA35288.1; -
DR InterPro; IPR006209; EGF like.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01186; EGF_2; 1.
SQ SEQUENCE 991 AA; 103024 MW; C51719B9F4D54A8E CRC64;
Query Match 46.6%; Score 54; DB 2; Length 991;
Best Local Similarity 56.2%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 GFCRCICTRGFCRCIC 16
DB 620 GFCSCICRNGFTGFNC 635
RESULT 12
Q9NRB6 PRELIMINARY; PRT; 174 AA.
AC Q9NRB6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mutant fibroblast growth factor receptor 3 (Fragment).
DE Names=FGFR3;
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```

RP SEQUENCE FROM N.A.
RA Chesi M., Brents L.A., Ely S.A., Bais C., Mesri E.A., Robbiani D.,
RA Kuehl W.M., Bergsgel P.L.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF238374; AAF97749.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 174 AA; 17810 MW; BC9917E34470B9EA CRC64;

Query Match 46.1%; Score 53.5; DB 2; Length 174;
Best Local Similarity 47.1%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 1 GFCRCICTRGFCRCICT 17
Db 75 GLCVCVCV---CVCVCT 88

RESULT 13
Q22048 PRELIMINARY; PRT; 164 AA.
AC Q22048;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein T01B7.8.
GN ORFNames=T01B7.8;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Sims M.A.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z66499; CAA91301.1; -.
DR PIR; T24272; T24272.
DR HSSP; P10969; 1K7V.
DR IntAct; Q22048; -.
DR WormBase; WBGene00011313; T01B7.8.
DR WormPep; T01B7.8; CE03592.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR006081; Defensin_alpha.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001007; VWF_C.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00269; DEFENSIN; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01208; VWFC_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 164 AA; 16499 MW; C002D48D36C9FCED CRC64;

Query Match 45.7%; Score 53; DB 2; Length 164;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICT 18
Db 80 GCGGCCCCPRCCCCRR 97

RESULT 14
Q95QV1 PRELIMINARY; PRT; 166 AA.
AC Q95QV1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein C04G6.10.
GN Name=C04G6.10; ORFNames=C04G6.10;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Anderson K., Chisoe S.;
RT "The sequence of C. elegans cosmid C04G6."
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U55854; AAK68159.1; -.
DR HSSP; P10969; 1WGT.
DR WormBase; WBGene00015458; C04G6.10.
DR WormPep; C04G6.10; CE27649.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR006081; Defensin_alpha.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001007; VWF_C.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00269; DEFENSIN; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01208; VWFC_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 166 AA; 16971 MW; 9D9D130351BB50F1 CRC64;

Query Match 45.7%; Score 53; DB 2; Length 166;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICT 18
Db 81 GCGGCCCCPRCCCCRR 98

RESULT 15
Q18238 PRELIMINARY; PRT; 188 AA.
AC Q18238;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein C27A2.5.
GN Name=C27A2.5; ORFNames=C27A2.5;

```

OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99089613; PubMed=9851916;
 RG WormBase Consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Nhan M.;
 RT "The sequence of C. elegans cosmid C27A2.";
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U58760; AAK31463.1; -.
 DR PIR; T15651; T15651.
 DR HSSP; P10968; 2CWG.
 DR IntAct; Q18238; -.
 DR WormBase; WEGene00016153; C27A2.5.
 DR WormPep; C27A2.5; CE04105.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR InterPro; IPR006081; Defensin_alpha.
 DR InterPro; IPR01007; VWF_C.
 DR PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
 DR PROSITE; PS00269; DEFENSIN; 1.
 DR PROSITE; PS01208; VWF_C_1; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 188 AA; 18878 MW; 0C5D0DC5CA8E0C4B CRC64;

Query Match 45.7%; Score 53; DB 2; Length 188;
 Best Local Similarity 50.0%; Pred.No. 18;
 Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GFCRCICTRGFCRCICTR 18
 | | | | | | | | | |
 Db 81 GGCGCCCCRPKCCCCCR 98

Search completed: April 28, 2005, 14:21:41
 Job time : 119 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2005, 13:57:35 ; Search time 122.5 Seconds
(without alignments)
56.830 Million cell updates/sec

Title: US-10-009-317A-33

Perfect score: 112
Sequence: 1 GVCRLCRGVGVCRLCRR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	18	4	AAB35047
2	112	100.0	18	5	ABP53296
3	112	100.0	18	8	ADO35231
4	112	100.0	18	8	ADO35242
5	112	100.0	18	8	ADO35241
6	107	95.5	18	8	ADO35243
7	102	91.1	18	5	ABP53298
8	99	88.4	18	4	AAB35030
9	99	88.4	18	5	ABP53297
10	99	88.4	18	6	AAB33866
11	99	88.4	18	7	ADP95202
12	99	88.4	18	8	ADP35357
13	99	88.4	18	8	ADG70012
14	99	88.4	18	8	ADO35229
15	99	88.4	18	8	ADO35238
16	99	88.4	18	8	ADO35239
17	99	88.4	18	8	ADO35256
18	99	88.4	38	8	ADO35263
19	95	84.8	18	4	AAB35037
20	92	82.1	18	5	ABP53294
21	92	82.1	18	6	AAB33801
22	92	82.1	18	6	AAB33863
23	92	82.1	18	8	ADN08176
24	89	79.5	18	5	ABP53299
25	89	79.5	18	6	AAB33804

26	89	79.5	18	6	AAB33864	Aae33864 Enantio-R
27	89	79.5	18	6	AAB33803	Aae33803 IGY retro
28	89	79.5	18	6	AAB33802	Aae33802 R9K retro
29	89	79.5	18	8	ADO35244	Ado35244 Rhesus th
30	89	79.5	18	8	ADN08177	Adn08177 Human ret
31	89	79.5	18	8	ADN08179	Adn08179 Human ret
32	89	79.5	18	8	ADN08178	Adn08178 Human ret
33	88	78.6	18	6	AAB33805	Aae33805 IZY retro
34	88	78.6	18	6	AAB33806	Aae33806 I11Y retr
35	88	78.6	18	8	ADN08180	Adn08180 Human ret
36	88	78.6	18	8	ADN08181	Adn08181 Human ret
37	86	76.8	18	4	AAB35046	Aab35046 Theta def
38	86	76.8	18	5	ABP53295	Abp53295 Anti-vira
39	86	76.8	18	6	AAB33865	Aae33865 RC-101/10
40	86	76.8	18	8	ADO35230	Ado35230 Rhesus th
41	86	76.8	18	8	ADO35255	Ado35255 Rhesus th
42	86	76.8	18	8	ADO35249	Ado35249 Rhesus th
43	85	75.9	18	6	AAB33807	Aae33807 R4Y retro
44	85	75.9	18	8	ADN08182	Adn08182 Human ret
45	84	75.0	18	8	ADO35254	Ado35254 Rhesus th

ALIGNMENTS

RESULT 1
AAB35047
ID AAB35047 standard; peptide; 18 AA.

AC AAB35047;

XX 27-MAR-2001 (first entry)

XX Theta defensin SEQ ID NO: 31.

XX Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan;
KW virus; helminth; disinfectant; food preservative; analogue.

XX Unidentified.

XX WO200068265-A1.

XX 16-NOV-2000.

XX 10-MAY-2000; 2000WO-US012842.

XX 10-MAY-1999; 99US-00309487.

XX (REGC) UNIV CALIFORNIA.

XX Selsted ME, Tang Y, Yuan J, Ouellette AJ;

XX WPI; 2001-031853/04.

XX Novel theta defensin peptide with antimicrobial activity against
bacteria, yeast, fungi, protozoa and viruses.

XX Claim 19; Fig 16; 110pp; English.

XX The present invention provides theta defensin peptides and analogues
which have antimicrobial activity. They can be used in the treatment of
bacterial, viral, fungal, protozoan and helminthic infections, in
disinfectants and as food preservatives

XX Sequence 18 AA;

Query Match 100.0%; Score 112; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 9.6e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVCRLCRGVGVCRLCRR 18

DB 1 GVCRLCRGVGVCRLCRR 18

Correct application
priority document

RESULT 2
ABP53296
ID ABP53296 standard; peptide; 18 AA.
XX AC ABP53296;
XX DT 13-NOV-2002 (first entry)
XX DE Anti-viral theta defensin peptide RTD-3 SEQ ID NO:29.
XX DE Anti-viral; viral infection; theta-defensin; lipid environment;
KW amphipathic alpha-helical structure; virucide; anti-HIV; immunisation;
KW viral growth inhibitor; viral proliferation inhibitor.
XX Macaca mulatta.
OS Synthetic.
XX WO200260468-A2.
XX PD 08-AUG-2002.
XX 29-JAN-2002; 2002WO-US002435.
XX 30-JAN-2001; 2001US-0265270P.
XX 01-AUG-2001; 2001US-0309368P.
XX (IOWA) UNIV IOWA RES FOUND.
XX Maury W, Stapleton J, Stinaki M, Roller R, Mccray PB, Tack B;
XX WPI; 2002-674815/72.
XX
XX New method of using a first anti-viral peptide comprising a Theta-
PT defensin peptide in an amphipathic Alpha-helical structure in a lipid
PT environment for reducing the infectivity of a virus.
XX
XX Disclosure; Page 10; 65pp; English.
XX
XX The present invention describes a method (M1) of using a first anti-viral
CC peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-
CC helical structure in a lipid environment for reducing the infectivity of
CC a virus. (I) can have virucide and anti-HIV activities, and can be used
CC to reduce virus growth, infectivity burden, shed, and development of anti
CC -viral resistance. (I) can be used for inhibiting the growth and
CC proliferation of a virus and so can be used for; (a) protecting or
CC treating subject from a viral infection, preventing recurrent viral
CC infection in a subject harbouring a latent virus, controlling virus
CC spread within a virally-infected subject (VS), reducing viral burden in a
CC VS, reducing virus shed from a VS, reducing percentage of VS in a
CC population regardless of viral infection status, or inducing latency in a
CC VS; (b) reducing the infectivity of a virus; and (c) rendering virus-
CC contaminated tissue or fluid sample safe for use, or reducing the number
CC of infectious virus particles in a population of viruses. (M1) is useful
CC for reducing the infectivity of a virus in sheep, cattle, horses, swine,
CC cats, fowl and humans e.g. an enveloped virus infecting humans such as
CC human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is
CC administered to a patient who is immunosuppressed or to a subject who is
CC not infected with the virus, where the first anti-viral peptide is
CC administered prior to or subsequent to the virus contacting the subject.
CC The anti-viral peptide is most preferably administered to a subject who
CC is chronically, latently or acutely infected with the virus. The present
CC sequence represents a rhesus monkey theta defensin anti-viral peptide,
CC which is given in the exemplification of the present invention
XX
XX Sequence 18 AA;
XX
XX Query Match 100.0%; Score 112; DB 5; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 9.6e-06;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GVCRCLCRGVCRCCLRR 18

Db 1 GVCRCLCRGVCRCCLRR 18
RESULT 3
ADO35231
ID ADO35231 standard; peptide; 18 AA.
XX AC ADO35231;
XX DT 15-JUL-2004 (first entry)
XX DE Rhesus theta defensin peptide, RTD-3.
XX DE Monkey; Rhesus theta defensin; RTD-3; antimicrobial peptide; cyclic;
KW antimicrobial; antiinflammatory; antibacterial; virucide; fungicide;
KW food; contact lens solution; eye wash solution; inflammatory response;
KW microbicidal inhibition; microbistatic growth inhibition; disinfectant;
KW food preservative; bacterial infection; viral infection;
KW fungal infection; haemolytic activity.
XX OS Macaca mulatta.
XX
XX Key Location/Qualifiers
FH Modified-site 1. .18
FT /note= "The peptide is cyclised by a covalent link
FT between these two residues"
FT Disulfide-bond 3. .16
FT Disulfide-bond 5. .14
FT Disulfide-bond 7. .12
XX US2004014669-A1.
XX 22-JAN-2004.
XX 30-APR-2003; 2003US-00427715.
XX 30-APR-2002; 2002US-0377071P.
XX (REGC) UNIV CALIFORNIA.
XX Selsted ME, Tran DQ;
XX WPI; 2004-167945/16.
XX Novel theta defensin analog useful for reducing or inhibiting growth or
PT survival of a microorganism in an environment such as food or food
PT product, contact lens solution, or eye wash solution, an inanimate
PT object.
XX
XX Example 1; SEQ ID NO 3; 46pp; English.
XX
XX The invention relates to a theta defensin analogue defined by formulae
CC detailed in the claims or appearing as ADO35231-ADO35257. The theta
CC defensin analogue is useful for reducing or inhibiting growth or survival
CC of a microorganism in an environment capable of sustaining the growth or
CC survival of the microorganism and is useful for reducing or inhibiting
CC growth or survival of a microorganism in an environment such as food or
CC food product, a solution (e.g., contact lens solution, or eye wash
CC solution), an inanimate object comprising surface, or a mammal. The
CC peptides are also useful for decreasing inflammatory response and for
CC microbicidal inhibition of survival of microorganism as well as
CC microbistatic inhibition of growth. Thus the peptides are useful as
CC therapeutic agents, disinfectants, food preservatives, or medicaments.
CC The peptides are also useful for treating a patient suffering from
CC bacterial, viral, fungal or other infection. The theta defensins have
CC high antimicrobial activity and low haemolytic activity. The present
CC sequence represents the rhesus monkey wild-type theta defensin RTD-3.
XX
XX Sequence 18 AA;
XX
XX Query Match 100.0%; Score 112; DB 8; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 9.6e-06;
XX

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVCRCRCRGVCRCLCRR 18
 Db 1 GVCRCRCRGVCRCLCRR 18

RESULT 4
 ADO35242
 ID ADO35242 standard; peptide; 18 AA.

AC ADO35242;

DT 15-JUL-2004 (first entry)

DE Rhesus theta defensin analogue peptide arTD-3-NH.

XX Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial;
 KW antiinflammatory; antibacterial; virucide; fungicide; food;
 KW contact lens solution; eye wash solution; inflammatory response;
 KW microbicidal inhibition; microbistatic growth inhibition; disinfectant;
 KW food preservative; bacterial infection; viral infection;
 KW fungal infection; haemolytic activity.

OS Macaca mulatta.

OS Synthetic.

FH Key Location/Qualifiers

FT Disulfide-bond 3. .16

FT Disulfide-bond 5. .14

FT Disulfide-bond 7. .12

FT Modified-site 18

FT /note= "Amidated"

US2004014669-A1.

22-JAN-2004.

30-APR-2003; 2003US-00427715.

30-APR-2002; 2002US-0377071P.

(REGC) UNIV CALIFORNIA.

Selsted ME, Tran DQ;

WPI; 2004-167945/16.

Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate object.

Claim 1; SEQ ID NO 16; 46pp; English.

The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.

Sequence 18 AA;

Query Match 100.0%; Score 112; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVCRCRCRGVCRCLCRR 18
 Db 1 GVCRCRCRGVCRCLCRR 18

RESULT 5

ADO35241
 ID ADO35241 standard; peptide; 18 AA.

AC ADO35241;

DT 15-JUL-2004 (first entry)

DE Rhesus theta defensin analogue peptide arTD-3-OH.

XX Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial;
 KW antiinflammatory; antibacterial; virucide; fungicide; food;
 KW contact lens solution; eye wash solution; inflammatory response;
 KW microbicidal inhibition; microbistatic growth inhibition; disinfectant;
 KW food preservative; bacterial infection; viral infection;
 KW fungal infection; haemolytic activity.

OS Macaca mulatta.

OS Synthetic.

FH Key Location/Qualifiers

FT Disulfide-bond 3. .16

FT Disulfide-bond 5. .14

FT Disulfide-bond 7. .12

FT Modified-site 18

FT /note= "Hydroxylated"

US2004014669-A1.

22-JAN-2004.

30-APR-2003; 2003US-00427715.

30-APR-2002; 2002US-0377071P.

(REGC) UNIV CALIFORNIA.

Selsted ME, Tran DQ;

WPI; 2004-167945/16.

Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate object.

Claim 1; SEQ ID NO 15; 46pp; English.

The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present

CC sequence represents a Rhesus theta defensin analogue peptide.

XX Sequence 18 AA;

Query Match 100.0%; Score 112; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVCRCRCRGVCRCRCRR 18
|||||
DB 1 GVCRCRCRGVCRCRCRR 18

RESULT 6

ADO35243
ID ADO35243 standard; peptide; 18 AA.

XX

AC ADO35243;

DT 15-JUL-2004 (first entry)

XX Rhesus theta defensin analogue peptide 3:1 ARTD-1-NH.

DE Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial;

XX antiinflammatory; antibacterial; virucide; fungicide; food;

KW contact lens solution; eye wash solution; inflammatory response;

KW microbicidal inhibition; microbistatic growth inhibition; disinfectant;

KW food preservative; bacterial infection; viral infection;

KW fungal infection; haemolytic activity.

XX Macaca mulatta.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 4. .17

FT Disulfide-bond 6. .15

FT Disulfide-bond 8. .13

FT Modified-site 18

FT /note= "Amidated"

FT

XX US2004014669-A1.

PN

XX

PD 22-JAN-2004.

XX

PF 30-APR-2003; 2003US-00427715.

XX

PR 30-APR-2002; 2002US-0377071P.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Selsted ME, Tran DQ;

XX

XX WPI; 2004-167945/16.

DR

XX Novel theta defensin analog useful for reducing or inhibiting growth or

PT survival of a microorganism in an environment such as food or food

PT product, contact lens solution, or eye wash solution, an inanimate

PT object.

XX

XX Claim 1; SEQ ID NO 17; 46pp; English.

PS

XX

CC The invention relates to a theta defensin analogue defined by formulae

CC detailed in the claims or appearing as ADO35239-ADO35257. The theta

CC defensin analogue is useful for reducing or inhibiting growth or survival

CC of a microorganism in an environment capable of sustaining the growth or

CC survival of the microorganism and is useful for reducing or inhibiting

CC growth or survival of a microorganism in an environment such as food or

CC food product, a solution (e.g., contact lens solution, or eye wash

CC solution), an inanimate object comprising surface, or a mammal. The

CC peptides are also useful for decreasing inflammatory response and for

CC microbicidal inhibition of survival of microorganism as well as

CC microbistatic inhibition of growth. Thus the peptides are useful as

CC therapeutic agents, disinfectants, food preservatives, or medicaments.

CC

CC The peptides are also useful for treating a patient suffering from
CC bacterial, viral, fungal or other infection. The theta defensins have
CC high antimicrobial activity and low haemolytic activity. The present
CC sequence represents a Rhesus theta defensin analogue peptide.

XX Sequence 18 AA;

Query Match 95.5%; Score 107; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVCRCRCRGVCRCRCRR 17
|||||

DB 2 GVCRCRCRGVCRCRCRR 18

RESULT 7

ABP53298

ID ABP53298 standard; peptide; 18 AA.

XX

AC ABP53298;

XX

DT 13-NOV-2002 (first entry)

XX Anti-viral chimeric theta defensin peptide H/RTD-3 SEQ ID NO:31.

XX Anti-viral; viral infection; theta-defensin; lipid environment;

KW amphipathic alpha-helical structure; virucide; anti-HIV; immunisation;

KW viral growth inhibitor; viral proliferation inhibitor.

XX Homo sapiens.

OS Macaca mulatta.

OS Synthetic.

XX WO200260468-A2.

PN

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PS Disclosure; Page 10; 65pp; English.

XX The present invention describes a method (M1) of using a first anti-viral

XX peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-

XX helical structure in a lipid environment for reducing the infectivity of

XX a virus. (I) can have virucide and anti-HIV activities, and can be used

XX to reduce virus growth, infectivity burden, shed, and development of anti

XX -viral resistance. (I) can be used for inhibiting the growth and

XX proliferation of a virus and so can be used for; (a) protecting or

XX treating subject from a viral infection, preventing recurring viral

XX infection in a subject harbouring a latent virus, controlling viral

XX spread within a virally-infected subject (VS), reducing viral burden in a

XX VS, reducing virus shed from a VS, reducing percentage of VS in a

XX population regardless of viral infection status, or inducing latency in a

XX VS; (b) reducing the infectivity of a virus; and (c) rendering virus-

XX contaminated tissue or fluid sample safe for use, or reducing the number

XX of infectious virus particles in a population of viruses. (M1) is useful

XX for reducing the infectivity of a virus in sheep, cattle, horses, swine,

XX cats, fowl and humans e.g. an enveloped virus infecting humans such as

XX human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is

XX

XX

XX

CC administered to a patient who is immunosuppressed or to a subject who is
 CC not infected with the virus, where the first anti-viral peptide is
 CC administered prior to or subsequent to the virus contacting the subject.
 CC The anti-viral peptide is most preferably administered to a subject who
 CC is chronically, latently or acutely infected with the virus. The present
 CC sequence represents a chimeric human/rhesus monkey theta defensin anti-
 CC viral peptide, which is given in the exemplification of the present
 CC invention

XX SQ Sequence 18 AA;

Query Match 91.1%; Score 102; DB 5; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00012;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVCRCCLRRGVRCICRR 18
 | : | | | | | | | | : |
 Db 1 GICRCCLRRGVRCICRR 18

RESULT 8
 AAB35030
 ID AAB35030 standard; peptide; 18 AA.

XX AC AAB35030;

DT 27-MAR-2001 (first entry)

XX Theta defensin SEQ ID NO: 1.

XX Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan;
 KW virus; helminth; disinfectant; food preservative; analogue.

XX OS Unidentified.

XX Key Location/Qualifiers

FT Cross-links 1. .18
 FT /note= "peptide bond cyclises the molecule"
 FT Disulfide-bond 3. .16
 FT Disulfide-bond 5. .14
 FT Disulfide-bond 7. .12

XX WO200069265-A1.

XX 16-NOV-2000.

XX 10-MAY-2000; 2000WO-US012842.

XX 10-MAY-1999; 99US-00309487.

XX (REGC) UNIV CALIFORNIA.

XX Selsted ME, Tang Y, Yuan J, Ouellette AJ;

XX WPI; 2001-031853/04.

XX Novel theta defensin peptide with antimicrobial activity against
 PT bacteria, yeast, fungi, protozoa and viruses.

XX Claim 4; Page 4; 110pp; English.

XX The present invention provides theta defensin peptides and analogues
 CC which have antimicrobial activity. They can be used in the treatment of
 CC bacterial, viral, fungal, protozoan and helminthic infections, in
 CC disinfectants and as food preservatives

XX SQ Sequence 18 AA;

Query Match 88.4%; Score 99; DB 4; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00024;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVCRCCLRRGVRCICRR 18

Db 1 GFCRCCLRRGVRCICTR 18
 | : | | | | | | | | : |

RESULT 9

ABP53297

ID ABP53297 standard; peptide; 18 AA.

XX AC ABP53297;

XX 13-NOV-2002 (first entry)

XX Anti-viral theta defensin peptide RTD-1 SEQ ID NO:30.

XX Anti-viral; viral infection; theta-defensin; lipid environment;
 KW amphipathic alpha-helical structure; virucide; anti-HIV; immunisation;
 KW viral growth inhibitor; viral proliferation inhibitor.

XX Macaca mulatta.

OS Synthetic.

XX WO200260468-A2.

XX 08-AUG-2002.

XX 29-JAN-2002; 2002WO-US002435.

XX 30-JAN-2001; 2001US-0265270P.

XX 01-AUG-2001; 2001US-0309368P.

XX (IOWA) UNIV IOWA RES FOUND.

XX Maury W, Stapleton J, Stinski M, Roller R, Mcray BB, Tack B;

XX WPI; 2002-674815/72.

XX New method of using a first anti-viral peptide comprising a Theta-
 PT defensin peptide in an amphipathic Alpha-helical structure in a lipid
 PT environment for reducing the infectivity of a virus.

XX Disclosure; Page 10; 65pp; English.

CC The present invention describes a method (M1) of using a first anti-viral
 CC peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-
 CC helical structure in a lipid environment for reducing the infectivity of
 CC a virus. (I) can have virucide and anti-HIV activities, and can be used
 CC to reduce virus growth, infectivity burden, shed, and development of anti
 CC -viral resistance. (I) can be used for inhibiting the growth and
 CC proliferation of a virus and so can be used for; (a) protecting or
 CC treating subject from a viral infection, preventing recurring viral
 CC infection in a subject harbouring a latent virus, controlling virus
 CC spread within a virally-infected subject (VS), reducing viral burden in a
 CC VS, reducing virus shed from a VS, reducing percentage of VS in a
 CC population regardless of viral infection status, or inducing latency in a
 CC VS; (b) reducing the infectivity of a virus; and (c) rendering virus-
 CC contaminated tissue or fluid sample safe for use, or reducing the number
 CC of infectious virus particles in a population of viruses. (M1) is useful
 CC for reducing the infectivity of a virus in sheep, cattle, horses, swine,
 CC cats, fowl and humans e.g. an enveloped virus infecting humans such as
 CC human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is
 CC administered to a patient who is immunosuppressed or to a subject who is
 CC not infected with the virus, where the first anti-viral peptide is
 CC administered prior to or subsequent to the virus contacting the subject.
 CC The anti-viral peptide is most preferably administered to a subject who
 CC is chronically, latently or acutely infected with the virus. The present
 CC sequence represents a rhesus monkey theta defensin anti-viral peptide,
 CC which is given in the exemplification of the present invention

XX SQ Sequence 18 AA;

Query Match 88.4%; Score 99; DB 5; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00024;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVCRCICRRGVCRCLCRR 18
 DB 1 GFCRCICRRGVCRICCTR 18

RESULT 10
 AAE33866
 ID AAE33866 standard; peptide; 18 AA.
 XX
 AC AAE33866;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Macaca mulatta RTDI peptide.
 XX
 KW Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV;
 KW human immunodeficiency virus; bacterial vaginosis; ophthalmic infection;
 KW antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1A;
 KW RTD1.
 XX
 OS Macaca mulatta.
 XX
 PN WO200285401-A1.
 XX
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US012353.
 XX
 PR 18-APR-2001; 2001US-0284855P.
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Lehrer RI, Waring AJ, Cole AM, Hong TB;
 XX WPI; 2003-103387/09.
 XX
 PT New isolated retrocyclin peptide, useful for preventing retroviral
 PT infections in cells susceptible to bacterial or viral infections or
 PT treating patients having the infections, such as HIV, sexually
 PT transmitted diseases, vaginosis.
 XX
 PS Example 1; Fig 3C; 72pp; English.
 XX
 CC The invention relates to novel retrocyclin peptides. Peptides and methods
 CC of the invention are useful for preventing retroviral infections in cells
 CC susceptible to bacterial or viral infections, or treating patients having
 CC infections such as HIV (human immunodeficiency virus), sexually
 CC transmitted diseases, bacterial vaginosis or ophthalmic infections. The
 CC retrocyclin-mediated killing is useful for modelling and screening novel
 CC antibiotics. The invention is also useful for gene therapy. The present is
 CC used in the exemplification of the invention
 XX
 SQ Sequence 18 AA;
 Query Match 88.4%; Score 99; DB 6; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00024;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GVCRCICRRGVCRCLCRR 18
 DB 1 GVCRCICTRGFCRCICRR 18

RESULT 11
 ADD95202
 ID ADD95202 standard; peptide; 18 AA.
 XX
 AC ADD95202;
 XX
 DT 29-JAN-2004 (first entry)
 XX

Cyclic defensin fragment.
 bacterial infection; human pathogen; holin; defensin;
 peptide nucleic acid; PNA; penicillin; tetracycline; ampicillin;
 kanamycin; antibiotic; antibacterial; antibiotic-resistance gene; cyclic.
 Unidentified.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..18
 FT /note="Residue 1 and residue 18 bond to form a cyclic
 moiety"
 FT
 FT Disulfide-bond 3..16
 FT Disulfide-bond 5..14
 FT Disulfide-bond 7..12
 XX
 PN WO2003059392-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 17-JAN-2003; 2003WO-DE000124.
 XX
 PR 18-JAN-2002; 2002DE-01001862.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Braun K, Braun I, Debus J, Pipkorn R, Waldeck W;
 XX WPI; 2003-689464/65.
 XX
 PT New conjugate of transport mediator and active agent, useful for treating
 PT prokaryotic infections, especially by neutralizing antibiotic resistance
 PT gene.
 XX
 PS Disclosure; Fig 10; 34pp; German.
 XX
 CC This invention describes a novel conjugate for treating prokaryotic
 CC infections which comprises a transport mediator for passage through the
 CC prokaryotic cell membrane and a compound, directed against a prokaryote
 CC and intended for introduction into it. The prokaryote is a bacterium,
 CC especially one pathogenic in humans. The transport mediator is preferably
 CC a human peptide or protein, especially a phage-holin protein, its active
 CC fragment or variant or a defensin. The introduced compound is a peptide
 CC nucleic acid (PNA) that inhibits a gene, especially one implicated in
 CC resistance to penicillin, tetracycline, ampicillin or kanamycin. The
 CC conjugate has the structure transport mediator-spacer-PNA where the
 CC spacer is poly(glycine and/or lysine), preferably containing 2-6 amino
 CC acids and the spacer is linked to the transport mediator through a
 CC cleavable disulfide bridge. The conjugates are administered together with
 CC an antibiotic, by parenteral, transdermal or subcutaneous routes. The
 CC products of the invention have antibacterial activity and are used,
 CC especially in combination with antibiotics, for treating prokaryotic,
 CC specifically bacterial, infections, especially where the pathogen is
 CC resistant to at least one antibiotic and then the PNA is directed against
 CC the antibiotic-resistance gene. Where the PNA is directed against an
 CC antibiotic resistance gene the conjugate will render the bacteria
 CC sensitive to co-administered antibiotics i.e. 'old' antibiotics can be
 CC used successfully in cases where normally they would be ineffective. This
 CC sequence represents a cyclic defensin fragment described in the
 CC disclosure of the invention.
 XX
 SQ Sequence 18 AA;
 Query Match 88.4%; Score 99; DB 7; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00024;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GVCRCICRRGVCRCLCRR 18
 DB 1 GFCRCICRRGVCRICCTR 18

RESULT 12

ADD35357
ID ADD35357 standard; peptide, 18 AA.
XX
AC ADD35357;
XX
DT 15-JAN-2004 (first entry)
XX
DE Antimicrobial peptide theta-defensin.
XX
KW antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological;
KW intraocular pressure; glaucoma; ocular hypertension; hyperaemia;
KW irritation; inflammation; conjunctiva; ocular cell dysplasia;
KW iridial melanocyte hyperplasia; hyperpigmentation.
XX
OS Unidentified.
XX
PN WO200307997-A2.
XX
PD 02-OCT-2003.
XX
PF 21-MAR-2003; 2003WO-US008935.
XX
PR 21-MAR-2002; 2002US-0367071P.
XX
PA (CAYM-) CAYMAN CHEM CO.
XX
PI Maxey KM, Johnson J;
XX
DR WPI; 2004-011506/01.
XX
PT Ophthalmic solution useful for the treatment of increased intraocular
PT pressure comprises a prostaglandin of the F-series and an antimicrobial
PT peptide.
XX
PS Disclosure; Page 11; 11pp; English.
XX
CC The invention relates to a novel ophthalmic solution comprising a
CC prostaglandin of the F-series and an antimicrobial peptide. A solution of
CC the invention has hypotensive and ophthalmological activity. The solution
CC is useful for the treatment of increased intraocular pressure, such as
CC caused by glaucoma and for the reduction of ocular hypertension. The
CC prostaglandin and the antimicrobial peptide work synergistically, to
CC provide beneficial reduction in the incidence of irritant and toxic side
CC effects such as hyperaemia, irritation and inflammation of conjunctiva,
CC ocular cell dysplasia, iridial melanocyte hyperplasia, and
CC hyperpigmentation, associated with the prior art prostaglandin
CC compositions. The present sequence represents an antimicrobial peptide of
CC the invention.
XX
SQ Sequence 18 AA;
Query Match 88.4%; Score 99; DB 8; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.00024;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 GVCRCLCRRGVCRCLCRR 18
Db 1 GFCRCLCRRGVCRICCTR 18
RESULT 13
ADG70012
ID ADG70012 standard; peptide, 18 AA.
XX
AC ADG70012;
XX
DT 11-MAR-2004 (first entry)
XX
DE Rhesus theta-defensin-1 (RTD-1) peptide.
XX
KW rhesus theta defensin-1; RTD-1; bacteraemia; lipopolysaccharide; LPS;
KW lipoteichoic acid; LTA; septic shock; antibacterial; fungicide; virucide;
KW immunomodulator; anticoagulant activity;
microbial cell-wall biosynthesis; immunomodulation; anticoagulant.
Macaca mulatta.
WO2003105883-A1.
24-DEC-2003.
30-MAY-2003; 2003WO-EP005694.
13-JUN-2002; 2002DE-01026216.
(FARB) BAYER HEALTHCARE AG.
Ladel C, Newton B, Labischinski H, Brunner N, Gerdes C;
WPI; 2004-071500/07.
Use of rhesus theta defensin-1 for treating or preventing bacteremia and
septic shock, also for binding bacterial products and as immunomodulator
and anticoagulant.
Example 1; SEQ ID NO 1; 28pp; German.
This invention describes the novel use of rhesus theta defensin-1 (RTD-1)
for preparing a composition for treatment and/or prevention of
bacteraemia for binding bacterial products such as lipopolysaccharide
(LPS) and/or lipoteichoic acid (LTA), or for treatment and/or prevention
of septic shock. RTD-1, isolated from immune cells of rhesus monkeys, has
antibacterial, fungicide, virucide, immunomodulator and anticoagulant
activity. RTD-1 inhibits microbial cell-wall biosynthesis and also binds
to LPS and LTA. RTD-1 is useful for treatment and prevention of severe
infections caused by Gram-positive or -negative bacteria and yeasts, or
by viruses. RTD-1 combines four advantageous properties: a direct
antimicrobial action, neutralisation of bacterial products (by binding),
immunomodulation (reducing release of proinflammatory cytokines but
increasing release of regulatory factors) and anticoagulant action, so
provides a better and simpler treatment.
Sequence 18 AA;
Query Match 88.4%; Score 99; DB 8; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.00024;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 GVCRCLCRRGVCRCLCRR 18
Db 1 GFCRCLCRRGVCRICCTR 18
RESULT 14
AD035229
ID AD035229 standard; peptide, 18 AA.
XX
AC AD035229;
XX
DT 15-JUL-2004 (first entry)
XX
DE Rhesus theta defensin peptide, RTD-1.
XX
KW Monkey; Rhesus theta defensin; RTD-1; antimicrobial peptide; cyclic;
KW antimicrobial; antiinflammatory; antibacterial; virucide; fungicide;
KW food; contact lens solution; eye wash solution; inflammatory response;
KW microbicidal inhibition; microbistatic growth inhibition; disinfectant;
KW food preservative; bacterial infection; viral infection;
KW fungal infection; haemolytic activity.
Macaca mulatta.
Key Location/Qualifiers
Modified-site 1..18
/note= "The peptide is cyclised by a covalent link
between these two residues"

FT Disulfide-bond 3. .16
 FT Disulfide-bond 5. .14
 FT Disulfide-bond 7. .12
 XX US2004014669-A1.
 PN XX
 PD 22-JAN-2004.
 XX
 PF 30-APR-2003; 2003US-00427715.
 XX
 PR 30-APR-2002; 2002US-0377071P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Selsted ME, Tran DQ;
 XX
 XX WPI; 2004-167945/16.
 XX
 XX Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate object.
 PT
 PT
 XX
 XX Example 1; SEQ ID NO 1; 46pp; English.
 PS
 CC The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-1.
 CC
 XX
 SQ Sequence 18 AA;
 Query Match 88.4%; Score 99; DB 8; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00024;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GVCRCRCRGVCRCRCRR 18
 Db 1 GFCRCRCRGVCRCICTR 18
 RESULT 15
 ADO35238
 ID ADO35238 standard; peptide; 18 AA.
 XX
 AC ADO35238;
 XX
 XX 15-JUL-2004 (first entry)
 XX
 XX Rhesus theta defensin analogue peptide aRTD-1-OH.
 DE
 XX Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; fungal infection; haemolytic activity.
 KW
 XX Macaca mulatta.
 OS
 OS Synthetic.
 XX

FH Key Location/Qualifiers
 FT Disulfide-bond 3. .16
 FT Disulfide-bond 5. .14
 FT Disulfide-bond 7. .12
 FT Modified-site 18
 FT /note= "Hydroxylated"
 XX
 XX US2004014669-A1.
 PN XX
 XX 22-JAN-2004.
 PD XX
 XX 30-APR-2003; 2003US-00427715.
 XX
 PR 30-APR-2002; 2002US-0377071P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Selsted ME, Tran DQ;
 XX
 XX WPI; 2004-167945/16.
 DR
 XX Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate object.
 PT
 PT
 XX
 XX Example 2; SEQ ID NO 12; 46pp; English.
 PS
 CC The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
 CC
 XX
 SQ Sequence 18 AA;
 Query Match 88.4%; Score 99; DB 8; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00024;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GVCRCRCRGVCRCRCRR 18
 Db 1 GFCRCRCRGVCRCICTR 18
 Search completed: April 28, 2005, 14:17:43
 Job time : 122.5 secs

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OM protein - protein search, using sw model

Run on: April 28, 2005, 14:12:37 ; Search time 30 Seconds
(without alignments)
44.789 Million cell updates/sec

Title: US-10-009-317A-33
Perfect score: 112
Sequence: 1 GVCRLCRRGVCRCLCRR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	88.4	18	3	US-09-309-487-1
2	99	88.4	18	4	US-09-967-808-1
3	95	84.8	18	3	US-09-309-487-9
4	95	84.8	18	4	US-09-967-808-9
5	92	82.1	18	4	US-10-141-645-1
6	89	79.5	18	4	US-10-141-645-2
7	89	79.5	18	4	US-10-141-645-3
8	89	79.5	18	4	US-10-141-645-4
9	88	78.6	18	4	US-10-141-645-5
10	88	78.6	18	4	US-10-141-645-6
11	85	75.9	18	4	US-10-141-645-7
12	80	71.4	18	4	US-09-917-340-53
13	77	68.8	18	4	US-10-141-645-8
14	77	68.8	18	4	US-10-141-645-9
15	62	55.4	92	3	US-09-309-487-22
16	62	55.4	92	4	US-09-967-808-22
17	62	55.4	141	4	US-10-141-645-68
18	62	55.4	141	4	US-10-141-645-72
19	61	54.5	140	4	US-10-141-645-66
20	61	54.5	141	4	US-10-141-645-67
21	60	53.6	76	3	US-09-309-487-16
22	60	53.6	76	4	US-09-967-808-16
23	60	53.6	76	4	US-10-141-645-17
24	60	53.6	92	3	US-09-309-487-21
25	60	53.6	92	4	US-09-967-808-21
26	60	53.6	141	4	US-10-141-645-73
27	58	51.8	17	3	US-09-604-864-1

28	58	51.8	17	4	US-10-042-872-1	Sequence 1, Appli
29	57	50.9	180	4	US-09-510-238A-286	Sequence 286, App
30	56	50.0	9	3	US-09-309-487-20	Sequence 20, Appl
31	56	50.0	9	4	US-09-967-808-20	Sequence 20, Appl
32	56	50.0	9	4	US-10-141-645-27	Sequence 27, Appl
33	56	50.0	9	4	US-10-141-645-45	Sequence 45, Appl
34	56	50.0	118	4	US-10-141-645-121	Sequence 121, App
35	56	50.0	140	4	US-10-141-645-69	Sequence 69, Appl
36	56	50.0	140	4	US-10-141-645-125	Sequence 125, App
37	56	50.0	141	4	US-09-252-991A-32502	Sequence 32502, A
38	55	49.1	168	4	US-09-270-767-40304	Sequence 40304, A
39	54.5	48.7	96	4	US-09-270-767-55820	Sequence 55820, A
40	54.5	48.7	96	4	US-10-141-645-33	Sequence 33, Appl
41	54	48.2	9	4	US-10-141-645-12	Sequence 12, Appl
42	54	48.2	59	4	US-08-999-811-4	Sequence 4, Appli
43	53.5	47.8	350	2	US-08-824-996-2	Sequence 2, Appli
44	53.5	47.8	350	2	US-09-042-105-4	Sequence 4, Appli
45	53.5	47.8	350	3		

ALIGNMENTS

RESULT 1
US-09-309-487-1
; Sequence 1, Application US/09309487
; Patent No. 6335318
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/309,487
; CURRENT FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-309-487-1

Query Match 88.4%; Score 99; DB 3; Length 18;
Best Local Similarity 83.3%; Pred. No. 9.3e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVCRLCRRGVCRCLCRR 18
| | | | | | | | | | | | | | | | | |
Db 1 GVCRLCRRGVCRCLCRR 18

RESULT 2
US-09-967-808-1
; Sequence 1, Application US/09967808
; Patent No. 6514727
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/967,808
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US/09/309,487
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18

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; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-967-808-1

Query Match      88.4%; Score 99; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 9.3e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVCRLCRRGVRCICRR 18
Db 1 GFCRLCRRGVRCICRR 18

RESULT 3
US-09-309-487-9
; Sequence 9, Application US/09309487
; Patent No. 6335318
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/309,487
; CURRENT FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-309-487-9

Query Match      84.8%; Score 95; DB 3; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.7e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVCRLCRRGVRCICLC 16
Db 3 GFCRLCRRGVRCIC 18

RESULT 4
US-09-967-808-9
; Sequence 9, Application US/09967808
; Patent No. 6514727
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/967,808
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US/09/309,487
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-967-808-9

Query Match      84.8%; Score 95; DB 4; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.7e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVCRLCRRGVRCICLC 16
Db 1 GFCRLCRRGVRCICRR 18

; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-967-808-1

Query Match      88.4%; Score 99; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 9.3e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVCRLCRRGVRCICRR 18
Db 1 GFCRLCRRGVRCICRR 18

RESULT 5
US-10-141-645-1
; Sequence 1, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-141-645-1

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Best Local Similarity 66.7%; Pred. No. 6e-05;
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QY 1 GVCRLCRRGVRCICRR 18
Db 1 GICRCICRGICRCICGR 18

RESULT 6
US-10-141-645-2
; Sequence 2, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-2

Query Match      79.5%; Score 89; DB 4; Length 18;
Best Local Similarity 61.1%; Pred. No. 0.00013;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVCRLCRRGVRCICRR 18
Db 1 GICRCICRGICRCICGR 18
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laps 0;

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laps 0;
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Db 1 GICICGRCGYCICGR 18

RESULT 15
 US-09-309-487-22
 ; Sequence 22, Application US/09309487
 ; Patent No. 6335318
 ; GENERAL INFORMATION:
 ; APPLICANT: Selsted, Michael E.
 ; APPLICANT: Tang, Yi-Quan
 ; APPLICANT: Yuan, Jun
 ; APPLICANT: Ouellette, Andre J.
 ; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
 ; FILE REFERENCE: P-UC 3095
 ; CURRENT APPLICATION NUMBER: US/09/309,487
 ; CURRENT FILING DATE: 1999-05-10
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 22
 ; LENGTH: 92
 ; TYPE: PRT
 ; ORGANISM: Macaca mulatta
 US-09-309-487-22

Query Match 55.4%; Score 62; DB 3; Length 92;
 Best Local Similarity 78.6%; Pred. No. 0.7;
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RCLCRGVCRCLCR 17
 Db 65 RCLCRGVCOLLR 78

Search completed: April 28, 2005, 14:23:42
 Job time : 30 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2005, 14:13:43 ; Search time 91 Seconds
(without alignments)
65.889 Million cell updates/sec

Title: US-10-009-317A-33

Perfect score: 112
Sequence: 1 GVCRCLCRRGVCRCCLRR 18

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Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	112	100.0	18	US-10-060-102-29	Sequence 29, Appl
2	112	100.0	18	US-10-427-715-3	Sequence 3, Appl
3	112	100.0	18	US-10-427-715-15	Sequence 15, Appl
4	112	100.0	18	US-10-427-715-16	Sequence 16, Appl
5	112	100.0	18	US-10-721-839-29	Sequence 29, Appl
6	107	95.5	18	US-10-427-715-17	Sequence 17, Appl
7	102	91.1	18	US-10-060-102-31	Sequence 31, Appl
8	102	91.1	18	US-10-721-839-31	Sequence 31, Appl
9	99	88.4	18	US-10-060-102-30	Sequence 30, Appl
10	99	88.4	18	US-10-313-994-1	Sequence 1, Appl
11	99	88.4	18	US-10-427-715-1	Sequence 1, Appl
12	99	88.4	18	US-10-427-715-12	Sequence 12, Appl
13	99	88.4	18	US-10-427-715-13	Sequence 13, Appl

14	99	88.4	18	15	US-10-427-715-30	Sequence 30, Appl
15	99	88.4	18	15	US-10-721-839-30	Sequence 30, Appl
16	95	84.8	18	14	US-10-313-994-9	Sequence 9, Appl
17	92	82.1	18	14	US-10-060-102-27	Sequence 27, Appl
18	92	82.1	18	14	US-10-141-645-1	Sequence 1, Appl
19	92	82.1	18	15	US-10-721-839-27	Sequence 27, Appl
20	89	79.5	18	14	US-10-060-102-32	Sequence 32, Appl
21	89	79.5	18	14	US-10-141-645-2	Sequence 2, Appl
22	89	79.5	18	14	US-10-141-645-3	Sequence 3, Appl
23	89	79.5	18	14	US-10-141-645-4	Sequence 4, Appl
24	89	79.5	18	15	US-10-427-715-18	Sequence 18, Appl
25	89	79.5	18	15	US-10-721-839-32	Sequence 32, Appl
26	88	78.6	18	14	US-10-141-645-5	Sequence 5, Appl
27	88	78.6	18	14	US-10-141-645-6	Sequence 6, Appl
28	86	76.8	18	14	US-10-060-102-28	Sequence 28, Appl
29	86	76.8	18	15	US-10-427-715-2	Sequence 2, Appl
30	86	76.8	18	15	US-10-427-715-14	Sequence 14, Appl
31	86	76.8	18	15	US-10-427-715-23	Sequence 23, Appl
32	86	76.8	18	15	US-10-427-715-29	Sequence 29, Appl
33	85	75.9	18	14	US-10-721-839-28	Sequence 28, Appl
34	85	75.9	18	14	US-10-141-645-7	Sequence 7, Appl
35	84	75.0	18	15	US-10-427-715-28	Sequence 28, Appl
36	81	72.3	18	15	US-10-427-715-19	Sequence 19, Appl
37	81	72.3	18	15	US-10-427-715-20	Sequence 20, Appl
38	81	72.3	18	15	US-10-427-715-31	Sequence 31, Appl
39	80	71.4	18	9	US-09-917-340-53	Sequence 53, Appl
40	80	71.4	18	17	US-10-844-837-53	Sequence 53, Appl
41	80	71.4	18	17	US-10-909-119-67	Sequence 67, Appl
42	77	68.8	18	14	US-10-141-645-8	Sequence 8, Appl
43	77	68.8	18	14	US-10-141-645-9	Sequence 9, Appl
44	76	67.9	18	15	US-10-427-715-37	Sequence 37, Appl
45	76	67.9	18	15	US-10-427-715-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1

US-10-060-102-29
; Sequence 29, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; US-10-060-102-29

Query Match 100.0%; Score 112; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GVCRCLCRRGVCRCCLRR 18

Db 1 GVCRLCRRGVCRCLCRR 18
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RESULT 2

US-10-427-715-3
; Sequence 3, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Thereof, and Methods of Use
; FILE REFERENCE: 66778-302(UC5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-427-715-3

Query Match 100.0%; Score 112; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GVCRLCRRGVCRCLCRR 18
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Db 1 GVCRLCRRGVCRCLCRR 18

RESULT 3

US-10-427-715-15
; Sequence 15, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Thereof, and Methods of Use
; FILE REFERENCE: 66778-302(UC5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-427-715-15

Query Match 100.0%; Score 112; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GVCRLCRRGVCRCLCRR 18
|||||
Db 1 GVCRLCRRGVCRCLCRR 18

RESULT 4

US-10-427-715-16
; Sequence 16, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:

; APPLICANT: Selsted, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Thereof, and Methods of Use
; FILE REFERENCE: 66778-302(UC5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: at the C terminus
US-10-427-715-16

Query Match 100.0%; Score 112; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GVCRLCRRGVCRCLCRR 18

RESULT 5

US-10-721-839-29
; Sequence 29, Application US/10721839
; Publication No. US20040086535A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
; TITLE OF INVENTION: CATHELICIDINS
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/721,839
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-721-839-29

Query Match 100.0%; Score 112; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GVCRLCRRGVCRCLCRR 18
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Db 1 GVCRLCRRGVCRCLCRR 18

RESULT 6
US-10-427-715-17
; Sequence 17, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Thereof, and Methods of Use
; FILE REFERENCE: 66778-302 (UC5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: at the C terminus
US-10-427-715-17

Query Match 95.5%; Score 107; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVCRLCRRGVCLCLR 17
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DB 2 GVCRLCRRGVCLCLR 18

RESULT 7
US-10-060-102-31
; Sequence 31, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-060-102-31

Query Match 91.1%; Score 102; DB 14; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.5e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVCRLCRRGVCLCLRR 18
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DB 1 GICRLCRRGVCLCGR 18

RESULT 8
US-10-721-839-31
; Sequence 31, Application US/10721839
; Publication No. US20040086535A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/721,839
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-721-839-31

Query Match 91.1%; Score 102; DB 15; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.5e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVCRLCRRGVCLCLRR 18
|:|||||||||:|
DB 1 GICRLCRRGVCLCGR 18

RESULT 9
US-10-060-102-30
; Sequence 30, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-060-102-30

Db 1 GFCRCLCRRGVCRCICTR 18
 Search completed: April 28, 2005, 14:26:50
 Job time : 91.5 secs

RESULT 14
 US-10-427-715-30
 ; Sequence 30, Application US/10427715
 ; Publication No. US20040014669A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sclated. Michael E.
 ; APPLICANT: Tran, Dat Q.
 ; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
 ; FILE REFERENCE: 66778-302(UC5754)
 ; CURRENT APPLICATION NUMBER: US/10/427,715
 ; CURRENT FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: US 60/377,071
 ; PRIOR FILING DATE: 2002-04-30
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 30
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic construct
 US-10-427-715-30

Query Match 88.4%; Score 99; DB 15; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e-05;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVCRCLCRRGVCRCIC 16
 | : ||||| ||||| : |
 Db 1 GICRCLCRRGVCRCIC 16

RESULT 15
 US-10-721-839-30
 ; Sequence 30, Application US/10721839
 ; Publication No. US20040086535A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MAURY, WENDY
 ; APPLICANT: STAPLETON, JACK
 ; APPLICANT: ROLLER, RICHARD
 ; APPLICANT: STINSKI, MARK
 ; APPLICANT: MCCRAY, PAUL B.
 ; APPLICANT: TACK, BRIAN
 ; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
 ; FILE REFERENCE: IOWA:0350S
 ; CURRENT APPLICATION NUMBER: US/10/721,839
 ; CURRENT FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: US/10/060,102
 ; PRIOR FILING DATE: 2002-02-22
 ; PRIOR APPLICATION NUMBER: 60/309,368
 ; PRIOR FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: 60/265,270
 ; PRIOR FILING DATE: 2001-01-30
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 30
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 US-10-721-839-30

Query Match 88.4%; Score 99; DB 15; Length 18;
 Best Local Similarity 83.3%; Pred. No. 9.7e-05;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVCRCLCRRGVCRCICRR 18
 | : ||||| ||||| : |

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 28, 2005, 14:00:51 ; Search time 26 Seconds
(without alignments)
66.612 Million cell updates/sec

Title: US-10-009-317A-33
Perfect score: 112
Sequence: 1 GVCRLCRGVCRCLCRR 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	71.4	18	2 C59089	theta defensin-1 -
2	60	53.6	76	2 B59089	theta defensin 1b
3	58	51.8	188	2 T15651	hypothetical prote
4	57	50.9	164	2 T24272	hypothetical prote
5	53.5	47.8	419	2 S69207	vascular endotheli
6	52.5	46.9	1131	2 T15617	hypothetical prote
7	52	46.4	152	2 T18975	hypothetical prote
8	51	45.5	76	2 A59089	theta defensin 1a
9	51	45.5	85	2 T48125	hypothetical prote
10	50.5	45.1	582	2 B45878	hypothetical prote
11	50	44.6	131	2 S50807	probable membrane
12	49.5	44.2	248	2 E71602	probable integral
13	49	43.8	476	2 JC5042	G protein-coupled
14	48	42.9	290	2 G72858	AcOrf-70 protein -
15	48	42.9	303	2 B70554	hypothetical prote
16	48	42.9	1217	1 EGMSMG	epidermal growth f
17	47.5	42.4	285	2 A41116	transcription fact
18	47	42.0	1700	2 S08167	Balbani ring 3 pr
19	47	42.0	2206	1 GNNY21	genome polyprotein
20	47	42.0	2910	2 T42214	otogelin - mouse
21	46.5	41.5	77	2 T48725	Q300 protein - mou
22	46.5	41.5	256	2 T46871	C-8 sterol isomera
23	46.5	41.5	835	2 JP0076	nel protein - chic
24	46	41.1	53	2 S29214	neurotoxin Tx2 - s
25	46	41.1	79	1 LNPGL	pulmonary surfacta
26	46	41.1	94	2 C37057	fibronectin recept
27	46	41.1	128	2 D72481	hypothetical prote
28	46	41.1	302	2 A25854	chloramphenicol re
29	46	41.1	321	2 H90942	probable diogenase

30	46	41.1	321	2 C64941	probable dioxygena
31	46	41.1	321	2 D85791	probable dioxygenase
32	46	41.1	484	2 C82426	cobyrinic acid synth
33	46	41.1	1133	1 EGR	epidermal growth f
34	46	41.1	1353	1 JH0675	restrictin precurs
35	45.5	40.6	83	2 S07405	proteinase inhibit
36	45.5	40.6	94	2 JC2225	Bowman-Birk protei
37	45.5	40.6	103	1 T15YC2	proteinase inhibit
38	45.5	40.6	532	2 T28784	hypothetical prote
39	45	40.2	95	2 S02186	hypothetical prote
40	45	40.2	321	2 AE0304	probable dioxygena
41	45	40.2	494	2 C70940	probable cobQ prot
42	45	40.2	602	2 H86468	protein F12K21.20
43	45	40.2	798	2 B27079	fibronectin recept
44	44.5	39.7	2946	2 T15840	hypothetical prote
45	44.5	39.7	118	2 S26689	hypothetical prote

ALIGNMENTS

RESULT 1

C59089
theta defensin-1 - rhesus macaque
N;Alternate names: RTD-1
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: C59089
R;Tang, Y.Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.
Science 286, 498-502, 1999
A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation
A;Reference number: A59089; MUID:99453140; PMID:10521339
A;Accession: C59089
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <SEL>
A;Note: this sequence is cyclically permuted by -6 residues from the sequence presented
C;Comment: For the two contributing precursor sequences, see PIR:A59089 and PIR:B59089.
C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing
F;1-9/Region: theta defensin 1a-derived
F;10-18/Region: theta defensin 1b-derived
F;1-18/Cross-link: cyclopeptide (Arg-Cys) #status experimental
F;2-11,4-9,13-18/Disulfide bonds: #status experimental
F;9-10/Cross-link: cyclopeptide (Cys-Arg) #status experimental

Query Match 71.4%; Score 80; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 0.0015;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RCLCRGVCRCLCRR 18
||:|||||
DB 1 RCICTRGFCRLCRR 15

RESULT 2

B59089
theta defensin 1b precursor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: B59089
R;Tang, Y.Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.
Science 286, 498-502, 1999
A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation
A;Reference number: A59089; MUID:99453140; PMID:10521339
A;Accession: B59089
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-76 <TAN>
A;Cross-references: UNIPROT:P82271; GB:AF191101; NID:96137229; PIDN:AAF04390.1; PID:961
C;Comment: For the complete mature sequence, see PIR:C59089.
C;Superfamily: mammalian defensin
C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing
F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-64/Domain: amino-terminal propeptide #status predicted <PRO>
F;74-76/Domain: carboxyl-terminal propeptide #status predicted <CTP>

Query Match 53.6%; Score 60; DB 2; Length 76;
Best Local Similarity 83.3%; Pred. No. 0.81;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RCLCRGVCRCL 15
|||||||:|
Db 65 RCLCRGVQCQL 76

RESULT 3

T15651

hypothetical protein C27A2.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T15651

R;Nhan, M.

submitted to the EMBL Data Library, May 1996

A;Description: The sequence of C. elegans cosmid C27A2.

A;Reference number: Z18382

A;Accession: T15651

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-188 <NHA>

A;Cross-references: UNIPROT:Q18238; EMBL:U58760; NID:g1330384; PID:g1330389; PIDN:AAB007

A;Experimental source: strain Bristol N2; clone C27A2

C;Genetics:

A;Gene: CESP:C27A2.5

A;Map position: 2

A;Introns: 19/3; 91/2

Query Match 51.8%; Score 58; DB 2; Length 188;
Best Local Similarity 55.6%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GVCRCLCRRGVCRCLCRR 18

|||||||:|

Db 81 GCGGCCCCRPKCCCCRR 98

RESULT 4

T24272

hypothetical protein T01B7.8 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T24272

R;Sims, M.

submitted to the EMBL Data Library, October 1995

A;Reference number: Z19867

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Accession: T24272

A;Molecule type: DNA

A;Residues: 1-164 <WIL>

A;Cross-references: UNIPROT:Q22048; EMBL:Z66499; PIDN:CAA91301.1; GSPDB:GN00020; CESP:T0

A;Experimental source: clone T01B7

C;Genetics:

A;Gene: CESP:T01B7.8

A;Map position: 2

A;Introns: 20/3; 90/2

Query Match 50.9%; Score 57; DB 2; Length 164;
Best Local Similarity 55.6%; Pred. No. 2.9;
Matches 10; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GVCRCLCRRGVCRCLCRR 18

|||||||:|

Db 80 GCGGCCCCRPKCCCCRR 97

RESULT 5

S69207

vascular endothelial growth factor C precursor - human

N;Alternate names: FLN4 ligand DHM

C;Species: Homo sapiens (man)

C;Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004

C;Accession: S69207; S61795; S71443; S69208; G02859

R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukkk, E.; Saksela,

EMBO J. 15, 1751, 1996

A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand f

A;Reference number: S69207; MUID:96203094; PMID:8612600

A;Accession: S69207

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-419 <JOU>

A;Cross-references: UNIPROT:P49767; EMBL:X94216; NID:g1177488; PIDN:CAA63907.1; PID:e22

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995

A;Note: only a part of the translation is shown

A;Note: this is a revision to the sequence from reference S61795

R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukkk, E.; Saksela,

EMBO J. 15, 290-298, 1996

A;Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (

A;Reference number: S61795; MUID:96178224; PMID:8617204

A;Accession: S61795

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 70-419 <JOU1>

A;Note: this sequence has been revised in reference S69207

A;Accession: S71443

A;Molecule type: protein

A;Residues: 'X', 104-120 <JOU2>

R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.

submitted to the EMBL Data Library, December 1995

A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and s

A;Reference number: S69208

A;Accession: S69208

A;Molecule type: mRNA

A;Residues: 1-419 <LEE>

A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989

R;Norris, J.C.

submitted to the EMBL Data Library, May 1996

A;Reference number: H01557

A;Accession: G02659

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-419 <MOR>

A;Cross-references: EMBL:U58111; NID:g1373426; PIDN:AAB02909.1; PID:g1373427

C;Genetics:

A;Gene: GDB:VEGFC; VRP

A;Cross-references: GDB:3890883; OMIM:601528

F;1-12/Domain: signal sequence #status predicted <SIG>

F;13-102/Domain: propeptide #status predicted <PRO>

F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>

Query Match 47.8%; Score 53.5; DB 2; Length 419;
Best Local Similarity 26.7%; Pred. No. 14;
Matches 8; Conservative 6; Mismatches 1; Indels 15; Gaps 1;

QY 3 CRCLCRGV-----CRCLCR 17

||:|:|:|

Db 291 CQCVCRAGLRPASCGRPHKELDRNSQCQCK 320

RESULT 6

T15617

hypothetical protein C5F6.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: T15617

R;Bentley, D.

submitted to the EMBL Data Library, October 1995

A;Description: The sequence of C. elegans cosmid C25F6.

A;Reference number: Z18377

A;Accession: T15617

A;Status: preliminary; translated from GB/EMBL/DDBJ

Db 65 RCICTRGFCRL 76

RESULT 9

T48125

hypothetical protein F16W2.210 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C/Accession: T48125

C/Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, submitted to the Protein Sequence Database, April 2000

A/Reference number: 224459

A/Accession: T48125

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-85 <RIE>

A/Cross-references: UNIPROT:O9M1V4; EMBL:AL138648

A/Experimental source: cultivar Columbia; BAC clone F16W2

C/Genetics:

A/Map position: 3

A/Introns: 20/1

A/Note: F16W2.210

Query Match 45.5%; Score 51; DB 2; Length 85;

Best Local Similarity 44.4%; Pred. No. 9.6;

Matches 12; Conservative 2; Mismatches 3; Indels 10; Gaps 2;

QY 1 GVCRCRCR----RGVC-----RCLCR 17

DB 52 GLCNLCRYGCAISGVCVSDPHRCRCR 78

RESULT 10

B45878

hypothetical protein 2 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C/Accession: B45878

C/Rsarvetnick, N.; Tsai, J.Y.; Fox, H.; Pilder, S.H.; Silver, L.M. Immunogenetics 30, 34-41, 1989

A/Title: A mouse chromosome 17 gene encodes a testes-specific transcript with unusual

A/Reference number: A45878; MUID:89307395; PMID:2568335

A/Accession: B45878

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-582 <SAR>

A/Cross-references: UNIPROT:Q62295; GB:M28821

A/Note: this sequence has been corrected in Immunogenetics 31, 283-284 (1990)

C/Superfamily: mouse hypothetical protein 2

Query Match 45.1%; Score 50.5; DB 2; Length 582;

Best Local Similarity 56.2%; Pred. No. 17;

Matches 9; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 2 VCRCLRRGVCRCLCR 17

DB 71 VCSMCVVYVCVCVCR 85

RESULT 11

S50807

probable membrane protein YUL064w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein HRC131; hypothetical protein J1120

C/Species: Saccharomyces cerevisiae

C/Date: 13-Jan-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004

C/Accession: S50807; S47126; S56838

C/RVandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F. Yeast 11, 57-60, 1995

A/Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisiae

A/Reference number: S50798; MUID:95282514; PMID:7762302

A/Accession: S50807

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A;Residues: 1-131 <VAN>
A;Cross-references: UNIPROT:P47038; EMBL:Z34288; NID:g498992; PIDN:CAA84058.1; PID:g49900
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
R;Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
A;Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisiae
A;Reference number: S47117
A;Accession: S47126
A;Molecule type: DNA
A;Residues: 1-131 <VAN>
A;Cross-references: EMBL:Z34288; NID:g498992; PID:g499002
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
A;Description: The protein sequence database, September 1995
A;Reference number: S56835
A;Accession: S56838
A;Molecule type: DNA
A;Residues: 1-131 <POH>
A;Cross-references: EMBL:Z49340; NID:g1008212; PID:g1008214; MIPS:YJL064w
C;Genetics:
A;Cross-references: SGD:S0003600
A;Map position: 10L
C;Superfamily: Saccharomycetes probable membrane protein YJL064w
C;Keywords: transmembrane protein

Query Match 44.6%; Score 50; DB 2; Length 131;
Best Local Similarity 52.9%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

QY 1 GVCRLCRRGVCRCLCR 17
DB 55 GTCCCC---CCCLCR 67

RESULT 12
E71602
probable integral membrane protein PFB0950w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C;Accession: E71602
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
; Perlea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: E71602
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-248 <GAR>
A;Cross-references: UNIPROT:O96282; GB:AE001428; GB:AE001362; NID:g3845316; PIDN:AACT197
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0950w

Query Match 44.2%; Score 49.5; DB 2; Length 248;
Best Local Similarity 46.7%; Pred. No. 28;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 2 VCRCLCRRGVCRCLC 16
DB 166 ICTCTC---ICSLC 177

RESULT 13
JC5042
G protein-coupled receptor - barnacle
C;Species: Balanus amphitrite (barnacle)
C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5042
R;Isola, A.; Kawahara, H.; Okazaki, Y.; Shizuri, Y.
Gene 175, 95-100, 1996
A;Title: Molecular cloning of a new member of the putative G protein-coupled receptor gene family from the barnacle Balanus amphitrite
A;Reference number: JC5042; MUID:97074655; PMID:8917082
A;Accession: JC5042

A;Molecule type: DNA
A;Residues: 1-476 <ISO>
A;Cross-references: UNIPROT:Q93126; DDBJ:D78363; NID:g1514430; PIDN:BAAL1375.1; PID:g1514430
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;34-57/Domain: transmembrane #status predicted <TM1>
F;71-93/Domain: transmembrane #status predicted <TM2>
F;107-129/Domain: transmembrane #status predicted <TM3>
F;126-134/Region: G protein-binding #status predicted
F;148-172/Domain: transmembrane #status predicted <TM4>
F;199-222/Domain: transmembrane #status predicted <TM5>
F;377-398/Domain: transmembrane #status predicted <TM6>
F;407-430/Domain: transmembrane #status predicted <TM7>
F;13.17/Binding site: carboxylate (Asn) (covalent) #status predicted
F;230.240.250.260/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;355/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted

Query Match 43.8%; Score 49; DB 2; Length 476;
Best Local Similarity 47.1%; Pred. No. 49;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 VCRCLCRRGVCRCLCR 18
DB 442 LCKCVCRCGAMERRRR 458

RESULT 14
G72858
AcOrf-70 protein - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A;Note: dsDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Accession: G72858
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus
A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Accession: G72858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-290 <AYR>
A;Cross-references: UNIPROT:P41470; GB:L22858; NID:g510708; PIDN:AAA66700.1; PID:g55913
C;Genetics:
A;Gene: AcOrf-70

Query Match 42.9%; Score 48; DB 2; Length 290;
Best Local Similarity 52.9%; Pred. No. 47;
Matches 9; Conservative 3; Mismatches 3; Indels 2; Gaps 2;

QY 4 RCLC-RRGV-CRCLCRR 18
DB 228 QCFCPRQGYKCEICRR 244

RESULT 15
B70554
hypothetical protein Rv1145 - Mycobacterium tuberculosis (strain H37Rv)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: B70554
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.;
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70554
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-303 <COL>
A;Cross-references: UNIPROT:O06545; GB:Z95584; GB:AL123456; NID:g3261774; PIDN:CAB09033
A;Experimental source: strain H37Rv

C:Genetics:
A:Gene: RV1145

Query Match 42.9%; Score 48; DB 2; Length 303;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 RCLCRGVCRCRCRR 18
|||
Db 281 RCCFRSPWRCRCRR 295
|||

Search completed: April 28, 2005, 14:22:38
Job time : 27 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2005, 13:58:25 ; Search time 114 Seconds
(without alignments)
80.855 Million cell updates/sec

Title: US-10-009-317A-33

Perfect score: 112
Sequence: 1 GVCRLCRRGVCRCLRR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_sprot;*

2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60.5	54.0	243	Q6ZMP3	Q6ZMP3 homo sapien
2	60	53.6	76	TD1B MACMU	P82271 macaca mula
3	60	53.6	168	Q9D912	Q9D912 mus musculus
4	58	51.8	168	Q6P8T4	Q6P8T4 mus musculus
5	58	51.8	168	Q8CH20	Q8CH20 mus musculus
6	58	51.8	173	Q9D4K2	Q9D4K2 mus musculus
7	58	51.8	188	Q18238	Q18238 caenorhabdi
8	57	50.9	164	Q22048	Q22048 caenorhabdi
9	57	50.9	166	Q950Y1	Q950Y1 caenorhabdi
10	57	50.9	197	Q17641	Q17641 caenorhabdi
11	57	50.9	274	Q949G1	Q949G1 oryza sativ
12	56.5	50.4	190	Q9U123	Q9U123 homo sapien
13	56.5	50.4	413	Q69566	Q69566 human herpe
14	55.5	49.6	512	Q6RY99	Q6RY99 rattus norv
15	55	49.1	201	Q6ZQ82	Q6ZQ82 homo sapien
16	54.5	48.7	212	Q7PDW6	Q7PDW6 anopheles g
17	54	48.2	212	Q7YUW7	Q7YUW7 caenorhabdi
18	54	48.2	905	Q8IH66	Q8IH66 drosophila
19	54	48.2	905	Q8IMJ2	Q8IMJ2 drosophila
20	53.5	47.8	379	Q7SXV0	Q7SXV0 brachydanio
21	53.5	47.8	418	Q57352	Q57352 coturnix co
22	53.5	47.8	419	1 VEGC HUMAN	P49767 homo sapien
23	53.5	47.8	419	Q6FH59	Q6FH59 homo sapien
24	53	47.3	307	Q9H9U3	Q9H9U3 homo sapien
25	53	47.3	881	Q9W0A0	Q9W0A0 drosophila
26	53	47.3	1823	Q7PRP5	Q7PRP5 anopheles g
27	52.5	46.9	101	Q7YU02	Q7YU02 trypanosoma
28	52.5	46.9	118	Q8C9N2	Q8C9N2 mus musculus
29	52.5	46.9	133	Q6R5G9	Q6R5G9 mus musculus
30	52.5	46.9	146	Q8BPC0	Q8BPC0 mus musculus
31	52.5	46.9	160	Q9H654	Q9H654 homo sapien

32	52.5	46.9	462	2	Q6GQP2	Q6GQP2 brachydanio
33	52	46.4	152	2	Q9XVX3	Q9XVX3 caenorhabdi
34	52	46.4	1506	2	Q8IRL0	Q8IRL0 drosophila
35	52	46.4	23015	2	Q8IQ18	Q8IQ18 drosophila
36	51.5	46.0	83	2	Q7PG24	Q7PG24 anopheles g
37	51.5	46.0	107	2	Q8BW14	Q8BW14 mus musculus
38	51.5	46.0	134	2	Q8N962	Q8N962 homo sapien
39	51.5	46.0	2327	2	Q9IBG7	Q9IBG7 xenopus lae
40	51	45.5	76	1	TD1A MACMU	P82270 macaca mula
41	51	45.5	85	2	Q9M1V4	Q9M1V4 arabidopsis
42	51	45.5	133	2	Q8HXJ6	Q8HXJ6 macaca fasc
43	51	45.5	628	2	Q8WGJ2	Q8WGJ2 sinorhizobi
44	50.5	45.1	94	2	Q8COH3	Q8COH3 mus musculus
45	50.5	45.1	96	2	Q6JMQ5	Q6JMQ5 burkholderi

ALIGNMENTS

RESULT 1

Q6ZMP3	PRELIMINARY;	PRT;	243 AA.
ID	Q6ZMP3		
AC	Q6ZMP3;		
DT	05-JUL-2004 (Tremblrel. 27, Created)		
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)		
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)		
DE	Hypothetical protein FLJ16784.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
ON	NCBI_TaxID=9606;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Tongue;		
RA	Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,		
RA	Wakabe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,		
RA	Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,		
RA	Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,		
RA	Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,		
RA	Wagatsuna M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,		
RA	Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahara K.,		
RA	Masuko Y., Nagai K., Isogai T.,		
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AK131548; BAD18682.1; -		
DR	HSSP; P09215; 1BDY.		
DR	GO; GO:0016301; P-kinase activity; IEA.		
DR	GO; GO:0007242; P.intracellular signaling cascade; IEA.		
DR	InterPro; IPR008973; C2_CaLB.		
DR	InterPro; IPR002219; DAG_PE-bind.		
DR	Pfam; PF00130; C1.1; 1.		
DR	PRINTS; PR00008; DAGPEDOMAIN.		
DR	SMART; SM00109; C1; 1.		
DR	PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.		
DR	Kinase.		
SQ	SEQUENCE 243 AA; 27566 MW; 23D41825EB9F782D CRC64;		

Query Match 54.0%; Score 60.5; DB 2; Length 243;
Best Local Similarity 66.7%; Pred. No. 3.1;
Matches 10; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY	2	VCRCLCRRGVCRCLC 16
		:
DB	177	VQCQLC---VCQCLC 188

RESULT 2

TD1B MACMU	STANDARD;	PRT;	76 AA.
ID	TD1B MACMU		
AC	P82271;		
DT	25-OCT-2004 (Rel. 45, Created)		
DT	25-OCT-2004 (Rel. 45, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Theta defensin-1, subunit B precursor (RTD-1b) (Demidefensin 1).		


```
SQ SEQUENCE 168 AA; 18931 MW; 7A2BD279612A5E94 CRC64;
Query Match 53.6%; Score 60; DB 2; Length 168;
Best Local Similarity 56.2%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CRCLRRGVCRCLCRR 18
||| ||| ||| |||
Db 66 CRCCCHCRCCRCRCSR 81

RESULT 4
Q6P8T4 PRELIMINARY; PRT; 168 AA.
AC Q6P8T4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 4931420D14Rik protein.
GN Name=4931420D14Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Xu X., Bai X., Silvius D., Escalier D., McFarland L., Xu P.-X.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF463502; AAO15675.1; -
DR MGD; MGI:1913992; 4931420D14Rik.
SQ SEQUENCE 168 AA; 18957 MW; 8F30D3D27B9BF595 CRC64;

Query Match 51.8%; Score 58; DB 2; Length 168;
Best Local Similarity 56.2%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CRCLRRGVCRCLCRR 18
||| ||| ||| |||
Db 66 CRCCCHCRCCRCRCSR 81

RESULT 6
Q9D4K2 PRELIMINARY; PRT; 173 AA.
AC Q9D4K2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4931420D14 product:hypothetical Cysteine-rich region
DE containing protein, full insert sequence.
GN Name=4931420D14Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Carninci P., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
```


DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01208; VWFC_1; UNKNOWN_1.
 KW Hypothetical protein.

SQ SEQUENCE 164 AA; 16499 MW; C002D48D36C9FCED CRC64;

Query Match 50.9%; Score 57; DB 2; Length 164;
 Best Local Similarity 55.6%; Pred. No. 6;
 Matches 10; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GVCRCLCRRGVCRCLCRR 18
 | | | | | | | | | |
 Db 80 GCGGCCCCPRCCCCRR 97

RESULT 9

ID Q95QY1 PRELIMINARY; PRT; 166 AA.
 AC Q95QY1; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein C04G6.10.
 GN Name=C04G6.10; ORFNames=C04G6.10;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99089613; PubMed=9851916;
 RG WormBase Consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Anderson K., Chisoe S.;
 RT "The sequence of C. elegans cosmid C04G6.";
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U55854; AAK68158.1; --
 DR HSP; P10969; IWGT.
 DR WormBase; WEGene00015458; C04G6.10.
 DR WormPep; C04G6.10; CE27649.
 DR InterPro; IPR001450; 4Fe4s_ferredoxin.
 DR InterPro; IPR006081; Defensin_alpha.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001007; VWFC.
 DR PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
 DR PROSITE; PS00269; DEFENSIN; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01208; VWFC_1; UNKNOWN_1.
 KW Hypothetical protein.

SQ SEQUENCE 166 AA; 16971 MW; 9D9D130351BB50F1 CRC64;

Query Match 50.9%; Score 57; DB 2; Length 166;
 Best Local Similarity 55.6%; Pred. No. 6;

Matches 10; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 1 GVCRCLCRRGVCRCLCRR 18
 | | | | | | | | | |
 Db 81 GCGGCCCCPRCCCCRR 98

RESULT 10

ID Q17641 PRELIMINARY; PRT; 197 AA.
 AC Q17641; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein C04G6.7.
 GN Name=C04G6.7; ORFNames=C04G6.7;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99089613; PubMed=9851916;
 RG WormBase Consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Anderson K., Chisoe S.;
 RT "The sequence of C. elegans cosmid C04G6.";
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U55854; AAK68161.1; --
 DR HSP; P10969; IWGT.
 DR WormBase; WEGene00015457; C04G6.7.
 DR WormPep; C04G6.7; CE27652.
 DR InterPro; IPR001450; 4Fe4s_ferredoxin.
 DR InterPro; IPR006081; Defensin_alpha.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001007; VWFC.
 DR PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
 DR PROSITE; PS00269; DEFENSIN; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01208; VWFC_1; UNKNOWN_1.
 KW Hypothetical protein.

SQ SEQUENCE 197 AA; 20596 MW; FB5F9457BFB9B8AD CRC64;

Query Match 50.9%; Score 57; DB 2; Length 197;
 Best Local Similarity 55.6%; Pred. No. 7;
 Matches 10; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GVCRCLCRRGVCRCLCRR 18
 | | | | | | | | | |
 Db 82 GCGGCCCCPRCCCCRR 99

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RESULT 11
ID Q949G1 PRELIMINARY; PRT; 274 AA.
AC Q949G1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Hypothetical protein C15ERIPDM.
GN Name=C15ERIPDM;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21329048; PubMed=11435398; DOI=10.1101/gr.GR-1617R;
RA Mayer K., Murphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T.,
RA Duysterhoeft A., Stiekema W., Entian K.D., Terry N., Lemcke K.,
RA Haase D., Hall C.R., van Dodeweerd A.M., Tingey S.V., Mewes H.W.,
RA Bevan M., Bancroft I.;
RT "Conservation of microstructure between a sequenced region of the
RT genome of rice and multiple segments of the genome of Arabidopsis
RT thaliana.";
RL Genome Res. 11:1167-1174(2001).
DR ENBL; AJ307662; CAC39030.1; -.
DR Gramene; Q949G1; -.
KW Hypothetical protein.
SQ SEQUENCE 274 AA; 28657 MW; AB547D9BD5470AE1 CRC64;

Query Match 50.9%; Score 57; DB 2; Length 274;
Best Local Similarity 60.0%; Pred. No. 9.3;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 RCLCRGVCRCRCRR 18
Db 185 RCCCHRGCCRCRAT 199

RESULT 12
ID Q9UI23 PRELIMINARY; PRT; 190 AA.
AC Q9UI23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Hypothetical protein C15ERIPDM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G.,
RA Zhang Y., Liu M., He F.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF111848; AAF16687.1; -.
SQ SEQUENCE 190 AA; 21480 MW; 4B8104A29AA33844 CRC64;

Query Match 50.4%; Score 56.5; DB 2; Length 190;
Best Local Similarity 55.6%; Pred. No. 7.8;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 2 VRCCLCRRG---VRCCLC 16
Db 47 VCLCMCVRGCVSVVCVC 64

RESULT 13
ID Q69566 PRELIMINARY; PRT; 413 AA.
AC Q69566;

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE U88.
GN Name=U88;
OS Human herpesvirus 6.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10368;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90112641; PubMed=2153237;
RA Littler E., Lawrence G., Liu M.Y., Barrell B.G., Arrand J.R.;
RT "Identification, cloning, and expression of the major capsid protein
RT gene of human herpesvirus 6.";
RL J. Virol. 64:714-722(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90080132; PubMed=2152817;
RA Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,
RA Barrell B.G.;
RT "Human herpesvirus 6 is closely related to human cytomegalovirus.";
RL J. Virol. 64:287-299(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91226542; PubMed=1851252; DOI=10.1038/351078a0;
RA Thomson B.J., Efstathiou S., Honess R.W.;
RT "Acquisition of the human adeno-associated virus type-2 rep gene by
RT human herpesvirus type-6.";
RL Nature 351:78-80(1991).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=91333007; PubMed=1651403;
RA Teo I.A., Griffin B.E., Jones M.D.;
RT "Characterization of the DNA polymerase gene of human herpesvirus 6.";
RL J. Virol. 65:4670-4680(1991).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374590; PubMed=1654446;
RA Martin M.E.D., Nicholas J., Thomson B.J., Newman C., Honess R.W.;
RT "Identification of a transactivating function mapping to the putative
RT immediate-early locus of human herpesvirus 6.";
RL J. Virol. 65:5381-5390(1991).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=91237802; PubMed=1851860;
RA Chang C.K., Balachandran N.;
RT "Identification, characterization, and sequence analysis of a cDNA
RT encoding a phosphoprotein of human herpesvirus 6.";
RL J. Virol. 65:2884-2894(1991).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=92148942; PubMed=1310766;
RA Geng Y., Chandran B., Josephs S.F., Wood C.;
RT "Identification and characterization of a human herpesvirus 6 gene
RT segment that trans activates the human immunodeficiency virus type 1
RT promoter.";
RL J. Virol. 66:1564-1570(1992).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=92260671; PubMed=1374813;
RA Neipel F., Eilinger K., Fleckenstein B.;
RT "Gene for the major antigenic structural protein (p100) of human
RT herpesvirus 6.";
RL J. Virol. 66:3918-3924(1992).

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RN [9] SEQUENCE FROM N.A.
 RP STRAIN=U1102;
 RC MEDLINE=92333249; PubMed=1321206;
 RX Bfstathiou S., Lawrence G.L., Brown C.M., Barrell B.G.;
 RA "Identification of homologs to the human cytomegalovirus US22 gene
 RT family in human herpesvirus-6";
 RT J. Gen. Virol. 73:1661-1671(1992).
 RL [10]
 RN [10] SEQUENCE FROM N.A.
 RP STRAIN=U1102;
 RC MEDLINE=93187613; PubMed=8383182;
 RX Ellinger K., Neipel F., Foa-Tomasi L., Campadelli-Flume G.,
 RA Fleckenstein B.;
 RT "The glycoprotein B homologue of human herpesvirus 6";
 RT J. Gen. Virol. 74:495-500(1993).
 RL [11]
 RN [11] SEQUENCE FROM N.A.
 RP STRAIN=U1102;
 RC MEDLINE=92333248; PubMed=1321205;
 RX Thomson B.J., Honess R.W.;
 RA "The right end of the unique region of the genome of human herpesvirus
 RT 6 U1102 contains a candidate immediate early gene enhancer and a
 RT homologue of the human cytomegalovirus US22 gene family";
 RL J. Gen. Virol. 73:1649-1660(1992).
 RN [12]
 RN [12] SEQUENCE FROM N.A.
 RP STRAIN=U1102;
 RC MEDLINE=93091236; PubMed=1333836;
 RX Compels U.A., Carss A.L., Sun N., Arrand J.R.;
 RA "Infectivity determinants encoded in a conserved gene block of human
 RT herpesvirus-6";
 RT DNA Seq. 3:25-39(1992).
 RL [13]
 RN [13] SEQUENCE FROM N.A.
 RP STRAIN=U1102;
 RC MEDLINE=94181269; PubMed=8134119;
 RX Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z.,
 RA Frenkel N., Rosenthal L.J.;
 RA "A transforming fragment within the direct repeat region of human
 RT herpesvirus type 6 that transactivates HIV-1";
 RL Oncogene 9:1167-1175(1994).
 RN [14]
 RN [14] SEQUENCE FROM N.A.
 RP STRAIN=U1102;
 RC MEDLINE=93224882; PubMed=8385692;
 RX Compels U.A., Carrigan D.R., Carss A.L., Arno J.;
 RA "Two groups of human herpesvirus 6 identified by sequence analyses of
 RT laboratory strains and variants from Hodgkin's lymphoma and bone
 RT marrow transplant patients";
 RL J. Gen. Virol. 74:613-622(1993).
 RN [15]
 RN [15] SEQUENCE FROM N.A.
 RP STRAIN=U1102;
 RC MEDLINE=93333202; PubMed=7687301;
 RX Pfeiffer B., Berneman Z.N., Neipel F., Chang C.K., Tirwatnapong S.,
 RA Chandran B.;
 RT "Identification and mapping of the gene encoding the glycoprotein
 RT complex gp82-gp105 of human herpesvirus 6 and mapping of the
 RT neutralizing epitope recognized by monoclonal antibodies";
 RL J. Virol. 67:4611-4620(1993).
 RN [16]
 RN [16] SEQUENCE FROM N.A.
 RP STRAIN=U1102;
 RC MEDLINE=93333170; PubMed=7687803;
 RX Pellett P.E., Sanchez-Martinez D., Dominguez G., Black J.B., Anton E.,
 RA Greenamoyer C., Dambaugh T.R.;
 RA "A strongly immunoreactive virion protein of human herpesvirus 6
 RT variant B strain 229: identification and characterization of the gene
 RT and mapping of a variant-specific monoclonal antibody reactive
 RT epitope";
 RL Virology 195:521-531(1993).
 RN [17]

RP SEQUENCE FROM N.A.
 RC STRAIN=U1102;
 RX MEDLINE=94025598; PubMed=8212582;
 RA Jones M., Teo I.;
 RT "Identification and analysis of the transport/capsid assembly protein
 RT (tp/cap) gene of human herpesvirus-6 (HHV-6)";
 RL Virology 197:449-454(1993).
 RN [18]
 RN [18] SEQUENCE FROM N.A.
 RP STRAIN=U1102;
 RC MEDLINE=93389439; PubMed=8397282;
 RX Liu D.X., Compels U.A., Nicholas J., Lelliott C.;
 RA "Identification and expression of the human herpesvirus 6 glycoprotein
 RT H and interaction with an accessory 40K glycoprotein";
 RL J. Gen. Virol. 74:1847-1857(1993).
 RN [19]
 RN [19] SEQUENCE FROM N.A.
 RP STRAIN=U1102;
 RC MEDLINE=94118404; PubMed=8289364;
 RX Nicholas J., Martin M.;
 RA "Nucleotide sequence analysis of a 38.5-kilobase-pair region of the
 RT genome of human herpesvirus 6 encoding human cytomegalovirus
 RT immediate-early gene homologs and transactivating functions";
 RL J. Virol. 68:597-610(1994).
 RN [20]
 RN [20] SEQUENCE FROM N.A.
 RP STRAIN=U1102;
 RC MEDLINE=94167865; PubMed=8122364;
 RX Zhou Y., Chang C.K., Qian G., Chandran B., Wood C.;
 RA "trans-activation of the HIV promoter by a cDNA and its genomic clones
 RT of human herpesvirus-6";
 RL Virology 199:311-322(1994).
 RN [21]
 RN [21] SEQUENCE FROM N.A.
 RP STRAIN=U1102;
 RC MEDLINE=95146989; PubMed=7844567;
 RX Compels U.A., Macaulay H.A.;
 RA "Characterisation of human telomeric repeat sequences from human
 RT herpesvirus-6 and relationship to replication";
 RL J. Gen. Virol. 76:451-458(1995).
 RN [22]
 RN [22] SEQUENCE FROM N.A.
 RP STRAIN=U1102;
 RC MEDLINE=94202288; PubMed=8151770;
 RX Thomson B.J., Dewhurst S., Gray D.;
 RA "Structure and heterogeneity of the a sequences of human herpesvirus 6
 RT strain variants U1102 and Z29 and identification of human telomeric
 RT repeat sequences at the genomic termini";
 RL J. Virol. 68:3007-3014(1994).
 RN [23]
 RN [23] SEQUENCE FROM N.A.
 RP STRAIN=U1102;
 RC MEDLINE=94202288; PubMed=8151770;
 RX Thomson B.J., Dewhurst S., Gray D.;
 RA "Structure and heterogeneity of the a sequences of human herpesvirus 6
 RT strain variants U1102 and Z29 and identification of human telomeric
 RT repeat sequences at the genomic termini";
 RL J. Virol. 68:3007-3014(1994).
 RN [24]

Query Match 50.4%; Score 56.5; DB 2; Length 413;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 10; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 2 VCCCLCRGVCRCIC 16
 Db 123 VCACLC---VCACLC 134

RESULT 14

Q6RY99 PRELIMINARY; PRT; 512 AA.
 ID Q6RY99
 AC Q6RY99;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Gamma-hydroxybutyrate receptor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Hippocampus;
RA Andriampandry C., Taleb O., Viry S., Muller C., Humbert J.P.,
RA Gobaille S., Anis D., Maitre M.;
RT "Cloning and characterization of a rat brain receptor that binds the
RT endogenous neuromodulator gamma-hydroxybutyrate.";
RL FASEB J. 0.0-0(2004).
DR EMBL; AY485933; AAR24072.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001209; Ribosomal S14.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR000301; Transmem_4.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00527; RIBOSOMAL_S14; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 512 AA; 56146 MW; 44DD12B937C40D60 CRC64;

Query Match 49.6%; Score 55.5; DB 2; Length 512;
Best Local Similarity 64.7%; Pred. No. 25;
Matches 11; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 2 VCRCLCRGVCRCLCR 18
DB 385 VCVCVCR-VCLCLCVR 400
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RESULT 15
Q6ZQS2 PRELIMINARY; PRT; 201 AA.
AC Q6ZQS2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ45585.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thalamus;
RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuno Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AKI28797; BAC87611.1; -.
DR InterPro; IPR006209; EGF like.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
SQ SEQUENCE 201 AA; 20938 MW; 3408F8E817AA0500 CRC64;

Query Match 49.1%; Score 55; DB 2; Length 201;
Best Local Similarity 53.3%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 VCRCLCRGVCRCLC 16
DB 58 VCLCVCLVSVCLCVC 72
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Search completed: April 28, 2005, 14:21:42
Job time : 115 secs

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